

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCTGCTGCCATCGTAGG  
ATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCCCTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTTCCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGTGTAA**TAA**CCCAATGTATCTGTGGGCCTATTCCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAAACACACCAATAGGCTGATTCAATCAAGATCCGTGCTGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCTATGTTAGATCG  
TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

**FIGURE 2**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLENYFSLNEKATNVFF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNTNYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRATNNQYEIV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGCGCGCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGAGGTAGAGAAAAGTCAGT  
 GCCACAGCCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGAGTCTGAGGGT  
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
 GCCGGGTAGGCTCTGGAAGGGGCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT  
 GTTCCCTCTTTCCGGGGTCTCTACCAGAAAGAGGTTCTTGGGGTTCGCCCTTCTGAGGAGGCT  
 GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG  
 GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTC  
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAAAACCTACCTAAATGATCGTCTTTG  
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
 CACATAGCCCACTTCTTAGGGAAGTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG  
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC  
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGAGACACACT  
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
 GAAAAGTGTTCGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
 TGATAAGATTTGATGTTTTTGGCTTGCTGTCATCTACTTTGTCTGGAATGTCTAAATGTTTC  
 TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRSLGQLLLTLEEIHAFGLTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRKKQNVDGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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**FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTACGCCATTGGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTTAACGGACTG  
CAAGATGAGGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCTGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCCTGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGTCTCTCCGCCAGAATTTCTCCGTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCTCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
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**FIGURE 6**

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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFERYHGLSSLCNLGCVLSNGLCLAGLALAIRSL

```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

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**FIGURE 7**

AATTCAGATTTTAAAGCCATTCTGCAGTGGAAATTTTCATGAAGTAGCAAGAGGACACCATCTT  
 CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT  
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG  
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 AGAATTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
 AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCCTGGGGT  
 CTGATCAATAATGCTGGTGTTCCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA  
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA  
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**FIGURE 8**

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MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGPHVIAACLT
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NDSLRRDMKAFGVHVSCEIEPLFKTNLADPVKVEKKLAIWEQLSPDIKQQYGEQYIEKSLD
KLKGNKSYVNMDLSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLKQK
AELANPKAV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCG**ATGGCT**GCGCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCGTGCACCACCT  
 GTAGTCATGTACCCACGCCGCCGCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGGCGCTCGTGCTGGAGGAAATGGA  
 AGCAACTGTGCAGATTGCAGCGGAATATGATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGT  
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAGCTCTGGCTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAATTTGCTGGGTTAAAACCAGCAAAATCCACCCGTCTTACCAG  
 CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCTGCACAGAAGACACAA  
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAGCCCTGTGGATCCCCGCCCGGAAGGAG  
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 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
 GAGGAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTTACACTTTGAAAGGACG  
 TGGACGTCAACCTGTTTGGAGGACAGCATCCGCATCCTGGGGGGGCTCCTGAGTGCCCTACCAC  
 CTGTCTGGGACAGCCCTTCTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC  
 CTTCAGAACACCATCCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC  
 CGCCACGCTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTAGCTGGAGTTCGG  
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAAGTGGAGAAGGTGACACAGGA  
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG  
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTGAGAAGCACTGCTGCGGCACCTCCGAGGCCAGTAAGCTCACTTTG  
 TGGGGGAGCTTGGCCACGGCCGCTTCAGTGCCAAAGATGGACCACCTGGTGTGCTTCTCGCA  
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGGCCAGGA  
 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGCTGAGTCCCGAGATCG  
 TGCATTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTTACCTGTACCGCTCACAGGGGA  
 CGCAAAATACCAAGACTGGGCTGGGAGATTCTGCAGAGCTTCAGGCCGATTCACACGGGTCC  
 CCTCGGCTGGCTATTCTCTCAACAATGTCCAGGATCCTCAGAACCCGAGCCTAGGAC  
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGTCTTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCTACGTGTTCAACACCGAAGCCCACTCTGCTTCTATCT  
 GGACCCCTGCC**TAGGGT**GGATGGCTGCTGGTGTGGGGACTTCAGAGCTGGCAGGACCTTG  
 CTGGTCTGTGGCATTITCCAAGGGCCACGTAGCACCGGCAACCGCAAGTGGCCAGGCT  
 CTGA**ACT**GGCTCTGGGCTCCTCTCGTCTCTGCTTAAATCAGGACACCGTGAGGACAAGTGA  
 GGCCCTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCGCTGGAGCCTCCGCTGCTTCTC  
 CAGAAGACACGAATCATGATCAGGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCGGACCA  
 GAGGGGGCTTCCAGGTGGTCCCTGGTACTGGGCTGACCGAGCTGAGCAGCTGCGAGTCTGAG  
 TCTGCCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGCTTGGAGGGGCTGCCGTGA  
 CTCAGAGGCTCTGAGGCTCAGGGCTGGCTCTGGTGTTCACAGCTGGACTCAGGGATCCTC  
 CTGGCGCCCGCAGGGGCTTGGAGGGCTGGACGGCAAGTCCGCTTACTAGCTACCGGCCCT  
 CCAGTGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTGTCTTAACGCCAA

**FIGURE 10**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSTFGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTISIQLFRELSTRLTGDKKFQEAWEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTFFVGEALHGRFSAKMDHLVCFPLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQGRRDVEVKPADRNLLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFENTEAHPLPIWTPA
```

**Important features of the protein:****Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
 CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
 AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC  
 CTGCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
 CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCCCCCCGTGCCTGCCCCCAGAG  
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCTGGGGCCCCACCCTGCGCAGTGTCTGGT  
 GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCTGTGCCACATGCGCCGCTTCCTGA  
 GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACAGGTGGACCACTTCAGGTTCAAC  
 CGGGCAGCGCTCATCAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC  
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
 CTGGGGCCGCGAGGACGACGAGTTCTACCGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC  
 GCCCTCGGGAATCACAACTGGGTACAAGACATTTGCCACCTGCATGACCCAGCCTGGCGG  
 AAGAGGGACCAAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC  
 CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
 AGC**TGA**GTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
 CAAGGCCTCAGTCTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
 AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACAGTGGG  
 GTGCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG  
 GGACCCCCCTGCCTTCTGCTCACCTTACTCTGACCTCCTTACGTGCCAGGCCTGTGGG  
 TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTTACTCTGACCTCCTTACGTGCC  
 AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSSRRKAAQLPWEDGRSGLSGGLPRKCSVFHLFVACLSTLGGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPPEPPPEHWEEDASWGPRLAVLVFFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVLLPLNEELDYGFPFAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

CAATGTTTGCCTATCACACCTCCCCAAGCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGAAGTGGTCGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCATCAGGGATTGGGCCTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCTCATCGGCCTGCCATGACCTGCAGCCAAGCCAGCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGCTTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTAAAGTGGTGTGTTATAGGCTATTACTAATTTATACAAAGATATTAAGGC  
CCTGTTCAATAGAAGATTGTCCCTTCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT  
AAATATGCTTTTATAATAAACAGTTAAAGCTGAAAAAAGGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ  
PRGEGEKVGDG

**Important features:****Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

14/249

GGACCCATGTCGGCGCGTGAACCCCGGCTCCCTAGAGGCCACGCGAGCCGACGGGACGAAAG  
GAGATATGTCGGCGCGCGGGGAGGCCCGCTCTCCGGCGCCATAGAGCTTCGGTTCGGCGCTGG  
CGCCGCGCCGCGCTCTTCCGCCCGCGGCTCCGGGCGCGCGCTAGGCACGTGCGCCGCCG  
CTCGCCCCGAGCGCCCCGGCCGCGAGCATGAGGCCACCGGACGCCGCGGGGCGCGCGCA  
GCCCGCGCTGTTGTCGCCGCTCTCGCTGCTTAGCGCTGCTCGCGCTGCTGGAGCCGCGCGCG  
CGCGCGCGCGCGCGCGCTGCCCGCGGCTGCAAGCACATGGCGGCCCGGAGGGGCTGGC  
AGGGCGCGCGGCGCGCCGAGGCGAAGGTGGTGTGCAGACGCTTGGAACTCGCGCAGGCTCC  
CGCCCCAGATACTCTGCCAACCGCACCTGATTTCTGATTAACATAAGATATCCT  
AGCTGAAGAATGGCTCATTTTTCTGGTTAAGTCTCTTTGAAGAGTTGGACCTCCGAAACAA  
CTTTATTAGTAGTATAGATCCAGGTCGCTTCTGGGACTGTCATCTCTAAAAGATTTGATCT  
GACAAACAATCGAATAGTAGTGTGTAATGCACATATTTTCAGGACTACCAATCTGGTTCT  
GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATATCTCAAGGAACCTTTTGATTATCTTCG  
TCATTACGGTCTTTTGGAAATCCAGACTGAGTATCTTTTGTGTGACTGAACATATCTGGAT  
GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGATACAGGTGTGTTTATCTAAGT  
CACTCAGGCCCCAACAGTACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCTCCGCTT  
GAATTCGCGCTCTTCTACATGATCCATCTCATCGCCAAAGTTGTGTTTGAAGGAGACAGCTT  
CTCTTTCAGTGCATGGCTCATATATTGATCAGACATGCAAGTGTGTGGTATCAGGAT  
GGAGATAAGTTGAAACCGATGAATCGCAAGGTATTTTGTGTTGAAAGAACATGATTACAACT  
TGTCCTTTGATTGCAAGTGCCCTAACCTTTCTAATATTACGCTGGATCTACTGGAAATTT  
GGGCTGTCACTGTCACAGCAAACGCTGGGAATAATCAGGAGACTGTGGATATTGTGGATTAG  
AGAGTTCTGCACAGTACTGTCTCCGAGAGGGTGGTAAACAAAGGCTGACTTCAGATGG  
CCGGAACAATTGCGAGGCATTACTGCATATCTGCAGTGTACGCGAACCCATGCGAGTGG  
GATATATCCCGGAAACCCACAGGATGAGAGAAAAGTTGGCGCAGATGTGATAGAGGTGGCT  
TTGGGCGAGATGATGATTATTTCTCGCTGTCAGTATGCAAAATGATCTCAGAGTTCTTTAT  
ATGTTTAAATCAGATGCCCTCAATCTTACCAATGCCGTGCCAACAGCTGCAGAGTTACTGCG  
TTACACTGTGGAAGCAGCCAACCTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA  
TTGAAAATTTTGAAGATTTTACAGAGGAGGAAAATCAAAGAGCTAGGTGACGTGATGGTT  
GACATTCGAAGTAACTATGCTGTGGCTGACAGCGTGTCTGTGGCTGGCGCAGAGGGAAGC  
TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCAATGCTACCTACCGGCTAGCCGGTG  
GAGCTCAGTTTTATCAACATATTCAACAAATTTGCTCTGGAAGCTTATGTCATCAAGTCT  
ACTGGCTTCACGGGGTAGCTCTGACCGTTCAGAAAGTGGCAGCTCTGATCGTACAGG  
ATTTCTCGAATTTGGGAGCGGGGATCCAGAGGGAACCTGGATTAAGACGTGAGCTTTAAGT  
GCAATGTTTCAAATACATTTTCGAGTCTGGCATAAAGTATGTTACATCTGCAATCATTT  
AAGACTATTTACAGTTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAAATACCTTATTA  
AAGAGATTTTTTTTCAGGAAGATAGGTATTTATGCTTTTGGTACTGTTTAAAGAAACATA  
ACAGGAAAGAACTGCAATTACAGCTTTCAAGGCCCTAGGCAATTTTGGCTTTTGAATCCCTTT  
CTTCACATAAAAAATACAGAATATACATTTTATAACTGCAGTGGTATTAATGCAAAATATACT  
ATTTGTACATGTGAAAATTTTTATTTGACTTAAAGATTTATTTATTTGTTTTTGTGCTCG  
GATTTAAGACATAAGATGTTTTTACGTGGCCCTCAAAGATATCATGAGCTTTTGGCAGTGC  
GCTTGGCCAAAGCCTAGTGGAGAAGTCAACCTGAGACCAAGTGTTAATCAAGCAAGCTGTAT  
ATCAAAATTTTTTGGCAGAAAACAAATATGTCATATCTTTTTTTAAAAAAGATTTTCA  
TTGAAGCAAGCAAAATGAAAGCATTTTTTACTGATTTTAAATTTGGTGCTTTAGATATATTT  
GACTACACTGTTATGAAGCAATAAGAGGAGGCAACACTCAGACCCCTAATGGAACCACTAT  
TTTTTCACTTAGCTTCTGTGGGACTGTGAATTGATTTCTTCGCGGTTTTTAACTTCACAG  
TACTTTATTTCTGTCTTTGTCCCTCAATAATACAAACAATATTCCAGTCAATTTTATGCT  
TGCATAATAACTGATCAACAGGTTGTAGTGTCTGGTTTAGTGTGAGCACTCAATAAATA  
TTGAATGAATGAACGAAAAAATAAAAAA

**FIGURE 16**

MEPPGRRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
 VVCSSELAQVLPDPTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
 FWGLSSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLEFQT  
 EYLLCDCNILLWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF  
 SHRQVVFEGLSLPFQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT  
 ISNIQAGSTGNWGVCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITA  
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLN  
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVMDIASNIMLA  
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
 VFQKVAASDRITGLSDYGRDRPEGNLDKQLSFKCNVSNTFSSSLALKVCYIILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
 433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
 384-390, 403-409, 554-560



**FIGURE 17**

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA  
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

"THE" SEQUENCE

## **FIGURE 18**

MSRSSKVVGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

10017306-123101

**FIGURE 19**

CTGTCGCTTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC  
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTCTCCGTGGATTCTCTGCTAAGACC  
 GCTGCC**ATG**CCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGG  
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCCGGGCCCTGACACAGCCCCGTTGGTCTCCTTCGC  
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCTGGAC  
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTCTGCTTCTCCGTGACCTGATCA  
 TCCTCATCGTGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC  
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC  
 CTATGTCCAGTTCCGTGCCACGGCCGTTTCGCGGGACACGCCATCGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCGGCCGCGAG  
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTACCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
 GAGTGCACCAACGTGTACCCATCCCTTCCCAGCTTCTGTGCGGGCTGGCCTTGTGTGTC  
 TGTCTCCTCTATGCCACCGCCCTGTGTTCTCTGGCCCTCTACCAGTTCGATGAGAAGTATG  
 GCGGCCAGCCTCGCGCTCGAGAGATGTAAGTGCAGCCGACGCCATGCCTACTACGTGTGT  
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGTCT**TAA**GACTCTCCCAAGAGGCTCC  
 CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
 TCCGCTTTCTCTGTTTTCTCTTCTGTCTCCCTCCCTCCACCTTTTTCTTTCTTCC  
 CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCTTCCCTTTCTCTGTGT  
 TTCCTTCTGTGTGTTTTGTTGCCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT  
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCCTCTGGGTTCAAGCGATTCTCCTCC  
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT  
 TTCCACTCTCTTTTTTCTCATCTCTTTCTGGGTTGCCTGTGCGGCTTCTTATCTGCCTGT  
 TTTGCAAGCACCTTCTCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCTCTGCTCCA  
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCCGTCCATGCCACAGCCCC  
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
 GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT  
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCTTTAAATTAATAAATATATATATATAT  
 ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCAGCCCTGGGTCCTTAGG  
 CCCCCTGCGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT  
 CTGTGGTATGAAAAAG

**FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727  
<subunit 1 of 1, 322 aa, 1 stop  
<MW: 35274, pI: 8.57, NX(S/T): 1  
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG  
SMGNWSMFTWCFCSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY  
VQFLSHGRSRDHAIATFFSCIACVAYATEVAVWTRARPGEITGYMATVPGLLKVLETFFVACI  
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIFPSPFLSGLALLSV  
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYVVCWDRRLAVAILTAINLLAYVAD  
LVHSAHLVFVKV

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21

[illegible]

**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLCS  
 LAWSFTRLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY  
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSSLCSLEDGLLGS PARLASQLLGDE  
 LLLAKLPPSRESAFRSLGLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
 QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
 285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCTCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT  
GGCACCCTCTGCTCAGTGCACATTTGTACACTTAACCCATCTGTTTCTCTAATGCACGA  
CAGATTCCCTTTCAGACAGGACAACATGTGATATTTCAAGTTCTGATTGTAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
TACAATCTATTCTTGCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACA**ATGT**TTGGCCTTAGCCAAAATTCGTTGATTTCACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGGAAGAAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
TTAAACAAATGAAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA  
GAAATATAACCACTCAAATCTCAAGCGGAGTCATTCCCTCGTTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCACATCTACCAATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCTT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCTGATA  
ACAGTTCCATTACAGTTAGCATCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAATTCAAACTCTTTCCAA  
ATACGTGAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTGCGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGAAAAAGGAAAAC  
GGATTCAATTTCCCATCGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT  
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCTATGGATGACATACC  
TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA  
CATCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT  
TCACCAATTACAGCCCTGCCTCATAACTAAATAATAAAAAATTTATCCACCAAAAAATCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAAATGAAGGGTGCTTTTTAAAGAAAAATTTGACTTAAAGCTAAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCTACCCAGGAAAGTAATAGCT  
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGCTCTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

**FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732  
><subunit 1 of 1, 334 aa, 1 stop  
><MW: 36294, pI: 4.98, NX(S/T): 13  
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA  
PIADEDLLPISAHPNATPALSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLTVGYLLCGKRKTD SFSHRRLYDDRNEFVLRLDNAPEPYDVSFGNSSYYNPTLNDSA  
MPSEENARDGIPMDDIPPLRTSV

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311



**FIGURE 25**

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCGAAGATTCACT**ATG**GTGAAAAATCGCCTTCAATACCCCTACCGCGGTGCAAAAGGAGG  
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
 TCATGCCCCAAGAGCACCATTTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA  
 AATTCCTTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTG<sup>1</sup>CAG  
 CAATTATTTCATGACTTTGAAAAGGGAATGACTGCCTTACCTGGACTTGTGTGCGGGAACTGC  
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG  
 CAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG  
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTATTTACCAACTTTGCAATAACAGA  
 AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**  
**AA**GAGGCAACAGATAGAGTGTCCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
 AAAAAAAGGAAAAAAAAAAAAAACTACTAACCACGCAAGCTCTTGTCAAATTTTAGTTTAAAT  
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG  
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCATCC  
 GTTGTTTTTTTTGTGTTGTTGTTTTCTTTCTTTAAGTAAGCTCTTTATTCATCTTATG  
 GTGGAGCAATTTTAAATTTGAAATATTTAAATTGTTTTGAACTTTTTGTGTAAATATA  
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTCATTTTGTACAACCTTCTTGAATTTAGA  
 AATTACATCTTTTCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG  
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCACAA  
 CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAA

**FIGURE 26**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSSGRCMLTLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDSPANLGRGEPNFLPVTEEADIREDDNIA
IIDVPVPFSFSDSDPAAIHDFEKGMTAYLDLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYPLPQTYVVRDELVAEEIRDVSNLGIIFYQLCNRKSFRLRRDLDLLGFKRAIDKCKWIR
HHPNEFIVETKIOAE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCAGAGCAGCCCCGGGCACACGACTCTCT  
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGCGGGGAGCACCCAGTCTGTACGCC  
 AAGAACTGGTCTGGGGGCACCATGGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCGCTCTGTGCCCTGAAGGCCACGTT  
 CCTGGAGGATGTGGCGGGTAGTGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
 CGCCACCTTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTGGGG  
 GGCCCATACCCCCCACCAACTTCTTGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCCGGGTCA  
 TCACCCGGCAGAAGCAGAAGGCCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC  
 GTGGACCAGAGTGACCGGGCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG  
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGACGGAGCCAGGATG  
 GTGGAGGCGAGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA  
 GGGACATGGGGTCCCAAGTGAGACACCAGAGGCGCAGGAGGACCGTCTCAGGGGTCCCTTG  
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCAG  
 GAAGCCCAGGGACCAAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG  
 TGTCTTAACAGTCTCCCGGGTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTCACTCCCC  
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCCTCCCTGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
 GGAATCTTACCAAGTGCCATCATCTTCACTCAGCAGCCCCAAAGGGCTACATCTACAGC  
 ACAGCTCCCTGACAAAGTGAGGGAGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTAAACAA  
 GCTACAGGGTAAAATCCTGCAGCACCCTCTGGAATACTGCTCTTAATTTTCTGAAGG  
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC  
 TCAAGCGCTCTCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
 GATCAGGTTGAATGAATGAACTCTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTTGAAGGGACCTCCACCTGGGGAAGTCCGAGGGGCTGGGAAGGGTTTCTGACG  
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG  
 TGTGCACAAATATTCGTAGTCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT  
 CTGGCAGGAGGTCTCTCCCCCATCCCTCCATCTGGGGCTCCCCCAAGCTCTGCACAGCTCT  
 CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAA  
 AAAGA

10017306.12401

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852  
><subunit 1 of 1, 283 aa, 1 stop  
><MW: 29191, pI: 4.52, NX(S/T): 0  
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL  
SPTSMGPQPTTLGGPSPTNFLDGI VDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA  
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP  
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE  
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

**FIGURE 29**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA  
GGGAGGACAGGGAGTTCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG  
GCAAGGAGGAGACCTTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATC  
AAGTTCCAGGGGGCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG  
CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC  
TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCAGCT  
GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG  
GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG  
CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCA  
GATGTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG  
AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG  
GTCTGGGACTCCGTGGGTCCACGGATACCCCGAAACTCAGCAGGCAGCTTTGGAATGAAT  
CCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC  
TCAGGGAGCTGTGGCCAGCCTGGCTATGTTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT  
GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC  
TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACATGGCAGCAGCAGTGG  
TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG  
GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCTCTCTGGGGA  
TCCAGCACCGGCTCCTCTCCGGCAACCACGGTGGGAGCGCGGAGGAAATGGACATAAACC  
CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGAGCGGGGAATCTGGGATTACGGGCTTCA  
GAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTGGGA  
GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT  
TGGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCT  
GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA  
AGCTCTCGCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACT  
CCCTCCTTAAACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTTGAATAAACCTTA  
GCTGCCCCACAA  
AAA

**FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWQGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGRGQGVSSNMREISKEGNRL
GGSGDNYRQGSSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKQ
RSSRIP
```

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

**FIGURE 31**

GACCGTGCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGGGCGGTGCTCACC  
 TCGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCTTGTCTGGAATATTACCGGGACATCTCA  
 CTCTCTGCTGCGCTGCACCGGAGCTTGGTTATGTGCGAGGAGAGTGAGGGGAAGATGTTGTTCTTGAAACAGC  
 TGTGTGCTACTTGTGCTCCTGGGCTGGCTTTCCAGATTCCCCAGTCCCTGAGGACTTGTCTTTCTTGGAAAGG  
 GTCCCTCATATGCCCTTGGAGTGACACAGTAGCCCCAGAGCATGGCTTGGACAATGGCCCTGTGGTGGACCAAGC  
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAATCTGCTCGCTTCGTGGGTGTGAGGAGTAGTG  
 GACGGAGTGGGGCTTCATGAGGAAATCACCCACCACCTACCAGGCTGAGGAGCCAGGCCTTCCAGACCA  
 GCCAGGGGCTCGAGGACAGCTCCGCCAGGCCCTTTTCCACAAACAGCCGCCCTCTCTGCGCCGAGCCGTAGAGT  
 TCGTGGCAGAAAGAAATTGGATCAAACTGTGTCAAACTATCAAGGCTACACTGGTGCGCAGATCTGGTGCGCCAGG  
 CAGAGTCACTTCTCCAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGCCAGCCAGCCAGCTGTTGGAGATCT  
 TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTTGCCCTTGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG  
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC  
 TTGCAACAGAGAAGCCTGTGCTTGGCTGTGAGCCAACATCACAGCAGTATCAGGAGGGAGGTGAAAGCAGCAG  
 TGAGTCGACACTTCGAGCCAGGGTCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGGCCCTGAGC  
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCCTGACAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC  
 CAGCTGGGCGAGCAGCTGCGGTGCCGCCAGTTCTGTGCCCACTGCTGAGCAGCATCTGGCAAAGTGTCTGTGT  
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAAATCTCTATCTAGGCCCCGGCACAGTACAGCTGGAGAGAGG  
 CAGGCTCGAAGGCTTCTGCACATCTGCTTCTCTTGTGGAAGGAAGACTTTCAGGGGCCGTTCCCTGCAGCTG  
 CTGCTGAGGCCAGAAATGTGGGCTTCTGGCAGACCAAGGCCAGGAGCTGGGACTTGTGCTGATTTCTTGCTA  
 CGSGAGCTGTTGGAGAAGGCTGTGATGGGACGGATCGAGATAGAGGCTGCTTGGCAGCCTCCACCAGGCCAG  
 TGGCCAGGGACTTTGCTGAGGAATTAGCAACACTGCTCATCTGTTCTAGGCCAGGCCCAAGCTGCCAGAACCC  
 CAGCTAAGAGCCTGTAGTTGGTGTCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGCTGAGAGATGGCC  
 CTGCTTGGGCAATTGACACAGAACCTTGGACCCCGGCTCAGGAGGAGGCCAAGTGCCCAATCGACAGCCTCAC  
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCTGCTGAGCATCCACACGCGA  
 ATCTATAGAGGAAGAGAGATTGGCCTGATTGGGATTATGGCAGAAAAGTCCACAGATGCCAGTCTGGAGTAGAA  
 GAGGTGGTGTGTTGTTATCTCTTGGTACTAAATGAAATGAGGTGTGGGGCTTGTCAACACAGATTCGAAGCT  
 CATTTGCTATCCAGCATCTCTAAACTTTGTAGTCTTGAATTCATGACAGAGCAAAATGACTCTGCTTAACT  
 TTATGAAGAAAGTTAAACATGAATCTTGGAGTCTACATTTCTTATCACAGGAGCTGGACTGCCATCTCCTT  
 ATAAATGCCATAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCAGCACTTTGAGAGGCTGAGGTGCGCG  
 GACTGCCCTGAGGTGAGGAATTCAGACACAGCCTGGCCAACTGGCAAAACCCATCTCTACTAAAAATAAAAAA  
 TTATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC  
 CTGGAGGTGGAGGTTGCAGTGAGCCGAGGTGCGACCACTGCCTCCAGTCTGGGTAAACAGAGCGAGACTTCTAG  
 AAAAAAGCTTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCGCCCTGTACCTTCAGCCCCTG  
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCAGCAGGGCAATTAGAGCTTTTAAAGATAAA  
 CTGGTTTTCTTAAAAAAGGGCTTTTATTAATAATTCTCCACACGATGGCTCTGCAATCTGCCACAGCTC  
 TGGGGCGTCTCCTGTAGGGAAGGCCCTGTTTCCCTGAGCGGGGCTGGGCTTGCCATGGTCCGCGGAGCTG  
 GCGGTCTGGCGCCCTGGCGTGTGCTAGCTGCTTCTGGCGGGCACAGAGCTGGGGGTCTGGGGGACCGGG  
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCTGCTCTTAACCGACACCTGAGGTGCTCCTGAGATGCTG  
 GGTCCACCTGAGTGGCACGGGAGGAGCTGTGGGCTGCTCCTCTYTAGGAGCTCCTGGGCAACTGAAGCTC  
 GGGCCCTCTTTTGCAGAGACCGAGGATGGGGTGGTGTGGGGGACTCATGGGAATGGCCTGAGGAGCTACGTGT  
 GAAGAGGCGCCGGTTTGTGGCTGTCAGCGGCTCTCCTGAGCCCTCAGTTTCCCTTCCGCTCTA  
 ATGAAGAATCATGCCCTCTCGGTGTCTCAGGGCTATTAGGACTTGCCTCAGGAAGTGGCCTTGGACGAGCGTAT  
 GTTATTTTCAAACTCTCTGACAGTGTGGCTGGGCACTCATGGAATGGCCATGTCTCCTCTGCTGCTGGTGGAC  
 GTGCGGCTGGGAGTGCAGCAGCAGAGGGCGGGGCGAGCAGTGCCTGGGCTGAGGGAGGAGGCCGCCGGGAGGG  
 CCTCAGGAAGTTGGGCTCCGCAACCAACAGCAGGCGGGGCTCCCGCGCGCCGCCACCCGCTCCAGG  
 GGCCGCTAGCAAAAGTGGAGTGCAGCTTGGCTCGCTGCGCAGCAGTAGCCCTTGATGCAGTGCGGACGCGG  
 TCGTCCCGAGCTGGAAGCAGCGCCGCTCCACCAACAGCAACAGCCGCTGCGCT

10017306-123101

**FIGURE 32**

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
 SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL  
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAGLATEKACAWLSANITAL  
 IRREVKA AVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282



**FIGURE 33**

TCCCTTGACAGGCTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCGAGCTTCCTTGAGGTGTGAACCCACATCCC  
 TGCCCCCAGGGCCACCTGACAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG  
 AGTAGCAACAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT  
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA  
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
 AACAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTGACAGCTCCAGCCACCTGCT  
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCCTACCGCGTCTCGTGCCCATTC  
 AGTGTGTTCCGCGTGCTGAGGAGGCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT  
 CATCTTCTGGGGGCCCGGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCTGTGATCC  
 AGCGAGCGGGCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCGCGCGCATGCGG  
 CAATTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGGTT  
 GAGCACAGGTGCTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCAAGTGCATGTCTATG  
 GCATGGTCCCCCAACTACTGACGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC  
 TACGAGCCCAAGGGGCCGACGAATGTGTACCTACATCCAGAATGAGCACAGTCCGAAGGG  
 CAACCACCACCGCTTCATACCCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA  
 TCACCTTCTCCCAACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG  
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATTCTTGCCCAATCAAGGCTTG  
 CTGGAGTGCTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCC  
 TGGGGAATCTGTTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
 TTGTGCAGTCAAGGCTGCGCACAGTCAATCAGGGTAGAGGGGTATTCTGAGTCAATCTG  
 AGGCTAAGGACATGTCTCTTCCATGAGGCCTGGTTTCAAGCCCCAGGAATGAGCCCCCA  
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTTGGTGTG  
 CCCCCTCAATTTCCAGCACCAAGAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC  
 GGCCAGAGAATTTGTGGGGTGTGTGAGGTTGTGGGGCGGTGGGAGGTCCAGAGGTGGGA  
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCTTCCCCCTCTCTGGG  
 CACCTTCTGCCACACCAAGTTTCCAGTGGGAGTCTGAGACCTTTCACCTCCCCACAA  
 GTGCCCTCGGGTCTGTCTCCCCGCTGTGACCTCCAGCCACTATCCCTTGCTGGAAGGCT  
 CAGCTCTTTGGGGGCTGTGGGGTGACCTCCCCACCTCCTGAAAACTTATAGGTATTTTTGC  
 GCAAACCTCTTCAAGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTCTGCCCT  
 CTAGCAGGAGGTTTTCCAACTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGCTCTCCCTCGACCTCTGTGCTCTGGGATGGCTGTCTGGGAGCTGT  
 ATCACTGGGTTCTGTCCCCGGCTCTGTATCAGGCATTTATTAAAGCTGGGCCCTCAGTGG  
 GGTGTGTTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
 GGCTGGAGGGACCAAGTGGAGGAGGCCAGCAGTAGCCATTGCACACTGGGGTGATGGGTGG  
 GGGCGGTGACTGCCACAGCTTGGTTTTGTAAATGATTGTACAGGAATAAACACACCTACGC  
 TCCGGA

**FIGURE 34**

MSSNKEQRSADVILFALITILILYSSNSANEVVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
 GNKTLPSRCHQCIVVSSSSHLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
 SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM  
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIARELCHVHVYGMVPPNYCSQRPRLQRMPIH  
 YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

## FIGURE 35

GTTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAAAGGAACTCAGCGGACCGGGAGCGGACGAGCTT  
 GAGGGAGAGCTCCCTAGCTGTTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGTGCGCCGAGAGTCTTGGAGGGCTGG  
 GCGAAGGTGCAAGACTTTTCAAGCAAGCTTCTCTGGACCCATGACCCCTTCTGCAAGCTTTCTGCAAGCTTTATACCGT  
 CTGAGGGTAGCAGCTCGAAGCTAGAAGAACTGGAGTCTTCCGAGGGACGGCAGTATCTCTTTGTGTGACCCTGCG  
 GCGCTATGGGAGCTTGGCTTCAGACCTTTGTGATACACCTGCTGCGTGGGACGATGACGGCGTGGAGAGGAAT  
 AGGCTCTGAGGTCACACTGGCTTGCCTCCTCTGATCAGCAGGCTGCTTTGCTGACTTGAACGAGGCTCCCTCAG  
 CTCACCGCTCAGGCTGGCTCCACGCTCCAGAAGCCGGGAGGCACTGTGATCTTGGGCTGGCTGGTGGAACTCCCA  
 AGGATGAATGTAACTTGGCCCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTTGGGTGTCTCTCATCACC  
 CACGGGACCCCTGCTCATCTACCTGCCCTTAACAACCCACACTGTGGGACGGTACCAAGTGTGGCCCGGATGCCCTGG  
 GGGCTGTGTGGCAGCGCTGCCAGCACTGTGACACTAGCCAACTCCAGGACTTCAAGTTAGATGTGCGACAGCTGT  
 ATTGAAGTGGATGAGGGAACACAGCAGTCTATGCTGCCACTGCTGAGAGGCCACCCCAAGCCCAAGCTGGCTGGG  
 TACAGGCTCAAAACAGAGTGGCTGGAGGCCCTCAGAGGTAACACTGCTATGCTTGGCTTCAAGGAACTCCAGATT  
 GTGAATGCCAGCCAGAGGAGCAGGGGATGTACAAGTGTGACGCTACAACCCAGTGAACCCAGAGTGAAGTGAAGAAC  
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC  
 CAACCATCATGCTCAGCAAGGCCAGAGTCTCATTTCTGGAGTGTGTGGCCAGTGGAACTCCACCCCCACGGGCT  
 CTTGGGCCAAGGATGGCTCAGTGTCAACGAGCGGCTTCTGTGTGAGAACCTCTCATCTGCAC  
 ACCACGAGCGAGGAGGACTCAGGCACTACCGCTGCAATGGCCGACAAATGGGTTTGGGCAAGCCGGGCGAGCGGCT  
 ATCTCTACAACTGTCCAGTGTGTTGAACCCCTGAGGTACCACTGAGCTATCCAGCTGCTCATCCCTGGGCG  
 CAGAGTGCACAGCTTCTGTGAGTGTGCTGGGAACCCCGGCTCCGCTGCTTGGCTGAGGAATCTGTGTGCC  
 CTATCTCCAGCAGGCTCTCCGCTCTCCGCAAGGCTCTGCGCTGCTCAGACTGGGGCTGAGGCAAGGCG  
 GTCTACCACTCATGTGGCCGAGAAGAGGTTGGGAGCGCCATGCGCTAGTCTGAGCTGCGGACCTCCAGGCCAAGC  
 ATAAACCCAGGCTGTGGCAGGATGCTGAGCTGGCTACTGGCACACTCTGTATACCCCTCCAACTCGGCAAC  
 CTGAGCAGACTGCTGAGGCGCAACCGGCGCTCCCGAGAGCCGCTCAGTGGGGCTGCTTCCCGAAGTGT  
 CCAGGAGAGAGGCGGAGGGGGCTCCCGCGAGGCTCCCATCTCTCAGCTCGCCCGCACTTCCAAAGACAGAC  
 TCTATATGAATGTTGTGGCGGCTCGCATGAGGCGATGGCGGGCGCCAACTCTCTATATCTGTGTGAAGAAC  
 CGCAAGCAGGTCACAAATTTCTCTGACGATTGGACCATCTCTGGACTTCCAGGCCAAGCAGACCGCTGACCCCT  
 ACCAAGTTGAACCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAATCTGTGGGAGAGGGCCAGACAGC  
 ATGGTCACCTTCCGAAGTGGACGGCGGCCAAACCCAGATCTATGGCCAGCAAGAGCAGGAGATCCAGAGAGAC  
 GACCCCTGAGCCGATCCCGAGAGCAGCAGCCAGCCAGCCAGCGCGCTCTCCCCCGCAAGACTTCCGAGCAGG  
 CCCACCATCTCCAGCGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTCCCAATC  
 CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGGCCACAGGCGCATCCCCCA  
 TCGCGGCTCTCCGTGGAGATCACGGGCTAGAGAAAGGCACTCTTACAAAGTTTCGAGTCCGGGCTCTGAACATG  
 CTCGGGAGAGCGCACTCCAGCCGCTCTCCGCGCTTACGTGTGTGCGGCTACAGGCTGCTGTGTACGAGAG  
 CCGCTGCGAGCTCTTATATCACTTCAAGTGTGCTCATGAGACCATCATCTCTCAAGTGGATGTACATC  
 CCAGCAGTAAACAAACACCCCAATCCATGGCTTTTATATCTATTTACAGCCACAGACAGTGAACATGATAGT  
 GACTACAAGAAGATATGTTGGAAGGGGCAAGTACTGGCACTCATCAGCAGCTCAGCCAGAGAGACTCTCTAC  
 GCAATTAAGATCAGTGTCTCAATGAAGGAGGGGAGGAGGATTCAGCAACGCTGATGATCTGTGAGACCAAGCT  
 CGGAAGTCTTCTTGGCCAGCTTGGTGCAGCTGCCACCCCACTCTGGCCCCACCAAGCCGCGCCCTTCTTGAACCC  
 ATAGAGCGCGCCGCTGGGCACTGGGCGCATGTTGGCTGCTTCCAGCGACCTGCGCTATCTGATTTGCGGGTCTGCT  
 CTGGGCTCATCTGTTCTCATCTGCTCAGCTTCTATCCCTCTGCTTGTGGAGGGCTGGTCTTAAGCAAAAACAT  
 ACAACAGACTGGGTTTCTCGAAGTGGCTTCCACCTCTTGGCCGCTATACATTTGTGCCATTGGGAGGACTC  
 CCAGGCCCCAGGCGAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGAGTCCACATG  
 AATAGGGGCTGCCCTCGGCTCGATGGGCTACCGGGGCTGAAGCCCCAGAGCATGTGCCAGGGCGAGCTTCAG  
 CAGCAGAGTGACACCCAGCGCTCTGAGGAGAGCCACTTGGCAATGGATATGACCCCAAGTCCACAGATC  
 ACAGGGGTTCCCAAGTCTAGCCCGGAGCGGGCTCTTCTTATACACACTGCCCCAGCTCCACTCACCAGCTG  
 CTCGACCCCTCATCAGCTGCTGACACCGCCAGGAGGAGCTGCTGCTGGGCGGAGTCCAGGGTGGAGAGAG  
 CCGCAGAGCTGCTCTGAGAGCTGTGGACCTCTGAGGCTCTGAGGCTCCCACTGAGGCTGTCTGGGCTGTG  
 CCAATTGAAGAGGTGACAGTCTGACTCTGCCAGTGAAGTGGAGGAGCTGGTGTCCCAAGCCCGGTAGG  
 GCTTACGTAGACAGCAACTGGATGACGCTCTCCCGGGCCACTGGTGGTGTGTCTTGAACACCACT  
 CTCACAAATTAGGCAGAAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAAAGAAAAA  
 AGAGACAGAAATATGGTATTATTTTTCTATTATAGCCATATTTATATATTTATGCACTTTGTAATATATGTA  
 TATGTTTTTATATTTCTGGAGAGACATAGGAGTCTTACCCGTTGAGGTTGGAGAGGAAAAAAGAAAGCTGCCA  
 CCTAACAGGAGTCAACCCAGAAAGCACCCGACAGGCTGGCGGGACAGACTCCTAACTGGGGCTCTGCAAGT  
 GCAGGCGAGGCTCGAGGAGGCCACAGATAAGCTGGCAAGGAGGAGATCCAGGACATGGTTTCATCAGGAGA  
 TGGAGGAACAGCAAGGGGACAGGATCACAGCTGGAGACCCACAGATGGCTGGATCCGGTGTCAAGCGAA  
 ACATTTTCTTAAGTATGCCATGAGAACAGACCAAGATGTGACAGCATATGAGCATTAAGAAACCTTCAGAAAT  
 CATAATCCGTGGCAACATATCTCTAAAAACAAACACTGTAACTTCAATAAATGTTTATCTTCCCTGTAAAA

**FIGURE 36**

MLRGTMTAWRGM RPEVTLACLLLATAGCFADLNEVPQVTVQ PASTVQKPGGT VILGCVVEPP  
 RMNVTVRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVI EVD EGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAARIIYPPEAQTI IVTKGQSL  
 ILECVASGIPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGGPGA  
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCM AENEVGS AHAVVQLRTSRPSITPRLWQDAELATGT PPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKGQGAPEAPIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE  
 TSVYVTWIPRNGGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV  
 RALNMLGESEPSAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIYPASNNNT  
 PIHGFYIYRPTDSDNDSDYKKDMVEGDKYWSISHLQPETSYDIKMQCFNEGGESEFSNV  
 ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPLYLVGVVLSIVL  
 IIVTFIPFCLWRAWSKQKHTDLDLGFP RSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPK  
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQEQA AVGQSGVRRAPDSPVLEAVWDPPFHS  
 GPPCCLGLVPVEEVDSPDCQVSGGDWCPQHPVGAYVQEPGMQLSPGFLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

**FIGURE 37**

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTGCGGCTCTGCCCATCGCCTGCTCCTC  
 CCAGGCTCCCGCGGCCGACCCCCGCGCAACATGCAGCCACGCGGCCGAGGGTTCCCGCGC  
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC  
 AGCCTCTTACCACGCGGGGTGTCCCCAGCGCCCTCACTACCCAGGCTCACTACGCCAGG  
 CACCCCCAAAACCTGGACCTTCGGGGTGC GCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
 TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
 TCGCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCTCCTACTCTGAAGTTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
 ACCTGACACTTACCTTCACCTGCAGTACCCATGGGCAGAGAGTTCACCAAGTTCAGACAC  
 CACATGTACACCAACGTGAGCGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGGCATGATGATAGATTTGTCTTATGCATCGGACACCTTGATAAGAAGGGTCTGG  
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
 TTGAATGTTCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGATTGGTGAAATATGACGGGACT  
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGGAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCCTGGAGGCTGAGTTT  
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCTCAGAATGGACACCAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCT  
 CCCCATACCTTGTTCAGGCTTGTGGCTGTGCCACCATCCCAACCTTCAACCCAGTGGCTC  
 TGTGACACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
 AGTTCAATTCACAAGCATATGCTGAGAATAACATGTTACACATGAAAA

10017306.423101

**FIGURE 38**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817  
 ><subunit 1 of 1, 487 aa, 1 stop, 2 unknown  
 ><MW: 53569.32, pI: 7.68, NX(S/T): 5  
 MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTAEETPGAPRALSTLGSPSLFTTPGVPS  
 ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ  
 TSLDRLRDGLVGAFWSASVSCSQSDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS  
 QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTFCSTPWAESSTKFRHHMYTNVSGLT  
 SFGEKVVEELNRLGMMIDLSYASDTLIRRVLVVSQAPVIFSHSAARAVCDNLLNVDPDDILQL  
 LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV  
 STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFPYGQLSTSCH  
 SHLV PQNHQATHLEVTKQPTNRVFWRSSNASPYLVPGLVAAATIPTFTQWLC

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGC**ATG**  
 AAGCTCTTATCTTTGGTGGCTGTGGTCCGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCAAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
 TTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTCATCATTTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC  
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG  
 TGTGGTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCCTT  
 CTCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
 GATCTCTGTGTCTTCTTGGGTCTTTGGGTTGAAGGAGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTCGAGGCGGCTCAGGAGTGGATGCGATCTGTCTCTCTGGCTCCACTCTTG  
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTCTTCA  
 GGAACCTCAGTGCTGGGAGGAAAGCATGCCCCAGCATTACAGCATGTGTTCTTTCTGCAGTG  
 GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCACTGGGTCTTCAGGGTGCAGTGGA  
 AGCTGGTGTTCGCTGTCCCTGTGCACCTTCTCGACTGGGCATGGAGTCCCCATGCATACT  
 CTGCTGCCGGTCCCCCTCACCTGCACCTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC  
 CACAGTCACTGAGCCAGACGCTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCACAGCCCTGTACTTGGGTGCCTCTTGTCCCTGAACCTTCGTTGTACCAAGTGCATGGA  
 GAGAAAATTTTGCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG  
 TTTTATTCTCTCA

**FIGURE 40**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHDEAYCLLCECRYEERSTTTIKVIIVIIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50



**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCGCCGA  
 ACCAGGAAGGGTTGAGGGAAACAATCTGCAAGCCCCGCGACCCAGTGGGGCCCCGCTGTTGGGGTCCTCCC  
 TCCTTTTGCAATTCACCCCTCCGGGCTTTCGCTCTTCCTGGGGACCCCTCGCCGGGAGATGGCGCGCTGTATG  
 CGGAGCAAGGATTCGTCTGTCTGCTCCTACTGCCCCGGTGTCTGATGGTGGAGAGCTCACAGATCGGCAGT  
 TCGGGGGCAAACTCAACTCCATCAAGTCTCTCGGGCGGGAGACGCTGGTCAGCGCCCAATCGATCTGGG  
 GGCATGTACCAAGGACTTGGCATTCGGCGGCAGTAAGAAAGGGCAAAACCTGGGGCAGCGCTACCCCTTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGGAGTATTGCCAGTCCCACCAAGGATCATCGGCTGCTGGTGTGTCGGAGA  
 AAAAAGAGCGCTGCCACGAGATGGCATGTGTCTGCCACAGTACCCGCTGCAATATATGGCATCTGTATCCGAGTT  
 ACTGAAAGCATCTTAACCCCTCACATCCCGCTCTGGATGGTACTCGGCACAGAGATCGAAACCGCGCTATTAC  
 TCAAAACATGACTTTGGGATGGCAGAACTAGGAAGACCAACACTAAGATGTACATATAAAGGGCATGAAGGA  
 GACCCCTGCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA  
 CCAGTGTCCATCAGGGGGAAGTCTGTACAAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT  
 TGGCACTGTGCGAAGGCGCTGTCTTGCAAAAGTATGGAAGATGCCACCTACTCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAATTTGATCACCATTGAGGAACATCATCAATTCAGACTGTGAAGTTGTGTATTTAATGCATTATAG  
 CATGGTGGAAAATAAGGTTGAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA  
 AAAGGGAGAAAGAAACATGAATGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG  
 CAACTTGTCTATGTAATAATGTACACATTTGGGAAAATGCTATTATTAAAGAGAACAGCACAGTGGAAAT  
 ACTGATGAGTAGCATGTACTTTCCAAGAGTTTAGGTTGTCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC  
 TTTATACAAATAACCTACATGCCAGATTTCTATTCAAGCTTAGAGTTTAAACAAATACTCCTAGAATAACTTGTTA  
 TACAATAGGTTCTAAAATAAAATTTGCTAAACAAGAAATGAAACATGGAGCATTTGTAATTTTACACAGAAAAAT  
 TACCTTTTGATTTCTAACACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT  
 TTTCCAAATTAATTTGCAAAATATGGCCAGTTGTTAGGAAGGCTTTAGGAAGACAAATAAATAACAAACAACAG  
 CCACAAATACATTTTTCAAAATTTAGTTTACCTGTAATATAAGAACTGATACAAAGCAACAAACAGTCTCC  
 TFCAGATTCTACGGAATGACAGTATATCTCTCTTATCTATGTGATTCTCGTCTGAATGCATTTATTTTCCA  
 AACTATACCCATAAATTTGACACTAGTAAAATCTTACACAGAGCAGAAATTTACAGATGCAGAAAAAATTTAAA  
 CATGTCCTAATATATGTGGGAAAAGAGTAAACAGAGATCATTTATTTCTTAAAGATTGGCCATAACTATATTTT  
 GATAGAATTAGATTGGTAAATACATCTATCATACACTCTGTGGTAAATAGAGACTTAAGCTGGATCTGTATCTG  
 CATCGGATTAAGCAAGAAAATTTGGGAAAATTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATCTCTG  
 AGGCACAAGTTGGCTGTTCTATCTTTGAAACCAAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT  
 CATATAATTTTACTATGAGATGAATCAGGTGAGGTCCTGTGTCGCTACTATCCTCAAAATTTATTTATTTATAG  
 TGTGAGATCTCAAAATAATCTCAATTTCAAGGAGTTTCAAAAAATGACTCCTGAAGTAGACAGAGTAGTGAGG  
 TTTGATTTGCCCTCTATAAGCTTCTGACTAGCCAAATGGCATCATCCAATTTTCTCCCAAGCCTCTGCAGCATCTG  
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCGAGCCATTGCGGTTAAAAAATAAAGTAGGATAAATTTGAAA  
 AACTGCAATTGCTAATCTATAGACACCAAGTTTCTAAATTTCTTGAACCACTTTTACTACTTTTTTAAACTT  
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAAATAAAGGTTATCTTATAGTCTGACTTTTAACTTTTG  
 TAGACCACAATTCATTTTATTTTCTTTTACTTAATCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG  
 AGATTGAGTTTGAGCCTGTATATCTATTTAAATTTCAACTTCCACATATATTTTACTAAGATGATTAAAGACTTA  
 CATTTTCTGCACAGGTCTGCAAAAAACAAAAATTATAAACTAGTCCATCCAAGAACCAAGTTGTATAAAGCAGT  
 TGTCTAAGCTTGTGAAATGAAATGGAACATTTCAATCAACATTTTCCATATATAACAAATTTATATATTTACAAT  
 TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTTATTTTGAAGTAAATTTTATACAGGAAATG  
 TTAATGAGATGATTTTCTATAGAGATATTTCTTACAGAAAGCTTTTAGCAGGAATATTTTGCAGCTATTGAC  
 TTTGTAATTTAGGAAAAATGTATAATAGATAAAATCTATTAATTTTCTCTCTCAAAAATCTGAAAAAATAA  
 AAAAAAAAAAAAAAAAAA

100730612301

**FIGURE 42**

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN  
GICIPVTESILTPHIPALDGTNRHRDRNHGHSNHDLGWQNLGRPHTKMSHIKGHEGDFCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

1007706.12301  
1007706.12301

**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA  
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT  
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
 TAGTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAAATCTTG  
**ATGTG**TTTTTAAAGCCTTGGGCAGAAATCTGTATTGTGAGGATTTGTTCTTTTATCCCCCT  
 TTTAAAGTCATCCGTCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAAATGGCAAACA  
 TCACCAGCTCCCAGATTTTGGACAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACTACTACTTCTTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCCTCAGTCCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT  
 CCTGGTTTGGAGTCCTTCTCTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAAATATCTCTGTGCTG  
 TCCACCAGCCACAGCCCAACACATCAAACCTTGCTAAGCGCGGATACCCCCAGCTTCTAAG  
 ATCCCAGCTTCTGCAGTGGAAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT  
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTCCCATCAGCTTGATTCTGAAGTCTTTAAGTGAGCCTTTGAATACA  
 TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCAATACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGTCCA  
 GGAACCATCATGAATGGACATGGTGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAACAGAGGAAGGATAGCTCACGTGA  
 TGTGGAACACACAGTTGGTCAATGGCTCATTCGTTAA~~AA~~AAAGCAGCCCTTTTGCTTTTGTG  
 TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT  
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC  
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAAACTC  
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCTGCCTGTAATCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

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**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT  
 TTGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACCTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCTGGAGGTACCCGACGGCCCCCGGCCACCCCGCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGGGCGCACCCGCGCTTCTGACCTGCGTGAACCGGGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCGGG  
 GTCCCGCACGACCGCGCGGACCGCTGCTGGACCTCTACGCGTCGGCGGAGCGCCGCGCCTA  
 CGGGCCCCCTTTTCTGCGCGACCGCGTGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCGGAACCCACGC  
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGGCGCCCAAGGCCACG  
 ACCCCACACTGGCGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCAC  
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTTTCATCCTGCTACTGGTCAC  
 TGTCTCTGGCCGCCCGCAGGCGCCCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGACGGGACCATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCGCGAAGGAGAACT  
 GCAAA**TAG**GGAGGCCCTGGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTGCGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCT  
 GGAATTTGGCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCCCTTGTCTACGGGTGGCCCTGCCACCCCTGGCACAACC  
 AAAATCCCACTGATGCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCTG  
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAAC**TGGGGT**CAGCCTCA  
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAACCTCGGCAGGAGTCCCACT  
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCAAGGACCTGTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTCTGCCCATCCCTACCCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT  
 GGACTCTGCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTGCCACTCTCAGACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCATCTGATTTTTAAAAA  
 AAAAA

**FIGURE 46**

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
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PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQV VHWDRQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGD FSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPGNGSSHS GAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKGDVNLA EFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAH SPLPAKYIDL DKGFRKENCK
```

**Important features:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGCGCGCTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT  
 CAGCACAGTTCAAACCTCCACCTACGGAACCAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAGCTGCTGGACCGCCGCCCTTGGCTGCAGAGGCCGAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTTACGCTGGGCATTGGCAGTCTACTGCCATGGAATCTCTTT  
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
 GGACCCTGAGGGCTCAGACATCCTGAACCTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
 TGCCCTCCATGCTGTGCTGGTGGCCAACCTCCTGCTTGTCAACAGGGTTGCAGTCCACATC  
 CGTGTCTCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCAGTGGTGAA  
 GGTGGACACTTCTCCTGGACCCGTGGTTTTTTTTGCGGTCACCATTTGCTGCATGGTGATCC  
 TCAGCGGTGCCTCCACTGTCTTACGACGAGCATCTACGGCATGACCGGCTCCTTTCTATG  
 AGGAACCTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
 ATTTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG  
 CCACCATCTTCTCTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCTGTCTTGGCGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA  
 GGACTCCCTCAGTGCCCTTTCGGTGGCCTCCAGATTATTGATTCCCAACACCCCTCTCC  
 GCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACCTACGCTTCTTCTCATACC  
 AGCCTCATCTACCCCGCCGCTGTCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACCTTTGCTGACCTAT  
 GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCAGGG  
 TTCGTGCTCCTCCGACCTGCCTCATCCCCCTCTTCTGTGCTCTGTAACCTACCAGCCCCGCT  
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG  
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTTACGGGCTTAAGATTGTGCCCAGG  
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG  
 CTCAGCCTGCTCTACCTCCTGGTGCACCTCATCT**TAGA**AGGGAGGACACAAGGACATTGGTG  
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGACAGGAGGGCTGGGGCCATGGAGGAAAGGCC  
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCAATTAACAGAACACT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
 ACATTCACCTTCTTCTAGCCCTCAAAGATGCTGCCAGTGTTGCGCCCTAGAGTTATTACA  
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCCTCATTTCCAGCT  
 GACAGCGAGATGCAAGCAAACTCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA  
 AGTCCCTGGCATGGTCAGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTCT  
 GCGGGTGAACAACTGCCCACTAACAGACTGGAAAACCCAGAAAGATGGGCCCTCCATGAAT  
 GCTTCATTCCAGAGGGACAGAGGGCCTCCCTGTGCAAGGATCAAGCATGTCTGGCCTGGG  
 TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTGGGTCAAGATGAGGCTC  
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCTAATAAATACTTGC  
 GTATTCAAAAA

**FIGURE 48**

MAVVEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYIIFFSLGI  
 GSLLPWNFFITAKEYWFMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
 LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGly  
 LLSRLEYARYYMRPVLAHVFSGEEELPQDSLAPSASVSRFIDSHTPPLRPILKKTASLGF  
 CVTYVFFITS LIYPAVCTNIESLNKGSGSLWTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
 GPNSKALPGFVLLRTCLIPFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
 305-330, 448-472

10017306-22101



**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGTGTCTGCTGTACCAAGAGCTGGAGACACCA  
 TCTCCACCGAGAGT**CATG**GGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCCTCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT  
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGCGCGGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC  
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCGAGAAGCTGGGCTACGCCTTGCCTCCCCAGGAAAAGGGCCACTCGCCCCAAGA  
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG  
 CGATGAAGAAGTTGAAAGGCACACGCTCTTGAATATCTTCTCGGGGAGGGGAACCTGAGC  
 CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCGAGGATGGCTTCTTCTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTTCTCGCCGCGCTGCCCGCCACATGCAGGAGGCGCTGCGGAGG  
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGAGGCCCTTCTGGCGCGAGGA  
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCGCTCGCGCATGATTTTCTACCGCGCGC  
 CGCGCGAGGGGCGCGTGTCTGCTGGCCTCGTACAGTGGTGGAGCGCGGCGGAGCGTTCCGC  
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
 TGTGCTGCCCAGCTCTGGGACGGCACCGGCGTCTGTCGAAGCGTTGGGCGGAGGACAGCACA  
 GCCAGGTTGGCTTTGTGGTACAGCCGCGGCGCTCTGGCAACCGAAAAGGATGACTGGACG  
 GTCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCGCTGCAT  
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGACAGGGCATGTGCATGGG  
 GTGGCCAGCAGCCCCTCGCATGACCTGGCAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG  
 CCAGTTATCTCTCAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGAAAAA  
 AA

**FIGURE 50**

MAPLALHLVLVPIILLSLVSQDWKAERSQDPFEKCMQDDPYEQLLKVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPPEKLGALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEGGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVMAMTQCPHDVHVQIETSPARNL  
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRFPFWREEHIEGG  
HSNTDRPSRMIFYPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIFYAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

**FIGURE 51**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT  
 GAGCGCTCTGAAAGCCACCTCTGTCTCTGGAGGAACACAGAGCGAGGGGAAGGACAGGAGCTCGTGTGGCAGGAA  
 GAACCTCAGAGCGCGGGAAGCCCCATTCTACTAGAAGCACTGAGAGATCGCGGCCCTCCGAGGGTCTGAAATTTCC  
 GCTGCTGTTTACAAAGATGCTTTTATCTTTTAACTTTTTGTTTTCCCACTCTCCGACCCCGGGCTTGATCTGCAT  
 CTTGACATTTGGAGCTGGCATCTTTCTTGTGGCTGATCACCAGACCTCAACCCGCTTTACCTCTCTTTGACCTGAA  
 CAATCAGTCTGTGGGAATTTGAGGGAGGAGCAGCGGAAGGGGTTTCCCAAGAAACAATGACCTTAAACAAGTTGCTG  
 CTTCTCAGATGCCAAGACTATGATGAGGTTTTCCAAAGAGGACTCGCTGTGCTGACAATGGGCCCTGCTTGGG  
 ATATAGAAAACCAAAACCGCCCTACAGATGGCTATCTTACAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTCT  
 CTGTCTCTTGATAAAGGTTATAAATCATCACAGACCACTTTGTGGGCTCTTTGCTCAGAATAGGCCAGAGTG  
 GATCATCTCCGAATTTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACAGGAAGC  
 CATCGTACATATTTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT  
 AGGGAATGTAGAGAAAGGCTTCAACCAGGCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA  
 GCAAGAGGGGGAGAAGTGAATTTGAGATCTTATCCCTATATGATGCTGAGAACCCTAGGCAAGAGCACTTCAG  
 AAAACCTGTGCCCTCTAGCCAGAAAGCTTGAGGCTCATCTGCTTCAACAGTGGGACCACAGGTGACCCCAAAGG  
 AGCCATGATAACCATCAAAATATTTGTTCAAATGCTGCTGCCCTTCTCAAATGTTGGAGCATGCTTTATGAGCC  
 CACTCCTGATGATGTGGCCATATCTTACCTCCCTCTGGCTCATATGTTTGAAGGATTGTACAGGCTGTTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
 CACATTTGTTTCCGCGGTGCCCTGCACTCCTTAACAGGATTCACGATTAAGGTACAAATGAGGCCAAGACACCTTT  
 GAAGAAGTTCTTGTGAAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
 TTTCTGGGACAAGCTCATCTTCTTGAAGATCCAGGACAGCTTGGGCGGAAGGGTTCGTGTAATTTGCTACCTGGGAC  
 TGCCCCATGTCACTTCACTGACATGACATCTTCCGGGCAACAAATGGGATGTCAGGTGTATGAAGCTTATGGTCA  
 AACAGAAATGCACAGGTGGCTGTACATTTACATTTACCTGGGACTGGACATCAGGTCAAGTTGGGCTGCCCTGGC  
 TTTGCAATTAAGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTTACAGTGAATTAAGAGAGAGGTGTGCTAT  
 CAAGGGTACAACCTGTTCAAAGATACCTGAAGGACCTTGAGAAGACACAGGAAGCCCTGGACATGATGGCTG  
 GCTTCAACAGAGGACATTTGGTGGCTGGCTCCGAAATGGAATCTGAAGATCATCGACCCTAAAAGAACAATTT  
 CAAGCTGGCCCAAGAGAGATTAATTCACACAGAGAAGATAGAAAATATCTACACAGAGAGTCAACCAAGTTTACA  
 AATTTTTGTACACGGGAGAGCTTACGGTCACTCCTTAGTAGGAGTGGTGGTTCCTGACACAGATGTACTCTCCCT  
 ATTTGCGACCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAGGGGAAGCACTTTT  
 AGAAGACTTGCAGAATTTGGGAAGAAAGTGGCCTTAAAACTTTTGAACAGGTCAAGGCCATTTTTTCTCATCC  
 AGAGCCATTTTTCCATTGAAAATGGGCTCTTGACACCAACATTTGAAGCAAGAGCGAGGAGAGCTTTTCCAATACTT  
 TCGGACCCAAATTTGACAGCCTGTATGAGCACATCCAGGATTAGTAGTAAGGTACTTAAGTACCTGCGCGCCCACTG  
 TGCACTGCTTGTGAGAAAATGGATTAAAAAATATTTCTACATTTGTTTTGCCCTTCCCTCATTTTTTTTTTAAAGC  
 TGTTAACTCTAAGAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAACTTAGTTCCCAATTAATCA  
 ATCCTGTCTTCCCATCTTCGATTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCCTGTCTTCAA  
 GATCCCAGTTTATGTTCTGTGCTTCTCATGATTTCCAACTTAACTATTTAGTAACCAAGTTCAAGGGT  
 CAAAGGACCCCTGTGGCTTCTTTGTTTTGTGATAAACATAACTTGCCAACAGTCTCATATGCTTATTTACA  
 TCTTTACTGTTCAACTAAGAGATTTTTAAATTTCTGAAAACCTGCTTACAATTCATGTTTTCTAGCCACTCCAC  
 AAACCACTAAAATTTTGTGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGCTCCGATGCTCTT  
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 CAGTAGGAAGTGGGAGTAAATCTGTGCTTCAAGTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
 GGTGGGCCCATGAACTTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCTGAACCTGGGAACAAAGATCT  
 ACAGGCAGCAAGATGCCACACAAAGGCTTATTTTCTGTGAAGGAACCACTGATCTCCCCACCCCTTGGATT  
 AGAGTTCTGCTCTACTTACCACAGATAACACATGTTGTTTCTACTTGAATAGTAAAGTCTTTAAAATAAAC  
 TATTACAGATAAAAAA

10017306.123101

**FIGURE 52**

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
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<MW: 82263, pI: 7.55, NX(S/T): 3
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CCFSDAKTMYEVEVQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKG YKSS
PDQVFVGIFAQNRPEWIISELACYTYSMAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLVKVIILMDPFDLQKQGEKSGIEILSLYDAENLGKEHFRKVPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFKCEVHAYEPTPDDVAISYLPLAHMFERIVQ
AVVYSCGARVGFQGDIRLLADDMKTLKPTLFFAVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTPLPGDWTSGHVGVPACNYVKLEDVADMNFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNIIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSSLVGVVVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSSIENGLLTPTLKA RGELSKYFR TQIDSLYEHIQD

```

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

**FIGURE 53**

GGAGGCGGAGGCCGCGGGCAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG  
 CCCGGGGCCCCCTAAGCCATTCTGAAATCATGGGCTGGCCAGGACATTGGTGAACCCGCCAAT  
 CCGGT**ATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAAGACGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGGCCCTGCGGAGATTCTGTCA  
 GACAGGGGCCGCTGCTTTCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCCTGGACA  
 CTCGGCGAGCCATCATGTGAAGCCAATGAAGACCCAGAGCCAGGACAAGCATGTGATGAGGCC  
 CTAGGCCGCTTGAGGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTCTGGACGTAGA  
 GGTGTATTCAAGTCGACGAAAGTATATGTGGCAGTGGATGGCACCACGGTCTCTGGAGGATG  
 AGGCCGGGAGCAGGGCCGGGGCATCCATGTCTATTGTCTCAACCAGGCCACGGGCCACGTG  
 ATGGCAAACGTTGTGTTGACAGCTACTACCTCATGAGGATGAGGCCATGGTGCTATTCTCT  
 CAACATGGTAGCGCCCGCGAGTGCTCATCTGCCTGTCAAGGATGAGGGCTCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCTGGGC  
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAGGAGGTCTGTCTTCGGGGAGAAACATTCT  
 TAAGTCACTGCCCTCTCTTCTGGGGGACCCAGTCTCTGCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCGCCGGCGCG  
 TTTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA  
 GTTCAGCCCTGACCCACTCCAGACAACAAGGTCTCAATGTGCTCTGGGCTGTCTATTGACG  
 GGAACCCAGCCAAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTACGCCACGGGGGTGCT  
 CCTCAGATGATAACAGTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGCACT  
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAAATGCCCCGCTGTCTCAGC  
 ACTCAAGGCCAGCCCTCACTGCCACTTTCAACCTGTTCCGGAGGCCAAGTTTGCTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTCAGTTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCCTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
 AGGAGGTCTCTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCATACACGGGAAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCGTAACAACGCCGGGGCCGAGAGTGCATCATCCTTGACG  
 TTTCCCGATCCTACCCTTTGGCATCGTCGGCTCAACATGAATGGCTACTTTACAGAGGCC  
 TACTTCAAGAAGCACAAGTTCAACACGGTTCACAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAAGAGCTTATGAAGTGAAGTTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCTTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTGGAATGGAGAAGATGATGACTTACCACCTGGACCCAGCTTGCCAAGTGCCCTACA  
 TATCTGGACCTGGATGTGCGTGCCGACCATCGGGGCTGTGGAGATTGTTTTCGGAAGAACA  
 ACCACTTCTGTTGGTGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGGCCACCTCAGTC  
 ACCCCAATTTTCTGGAGCCACCCCAAGAGGAGGGAGCCCCAGGAGCCCAGAACACAGAC  
**ATGAC**ACTCTCTCGAGGACCTGCGGGCTGGGTACTGTGTACCCCAAGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGCTGGGGCTACCTTGTTTTAAACA  
 TGAGACTTAATTACTAATCCAAGGGGAGGGTTCCCTGCTCCAACACCCGTTCTCGAGTT  
 AAAAGTCTATTTATTTACTCTTCTGTTGGAGAAGGCGAGAGAGTACTGGGAATCATTACG  
 ATCCCTGACAGCTCATCTGCCCTTTGTAATACCTCACTTCCAGGCCCTGGCTCAGAATTCA  
 ACCATTATTAGACTGTCTGAGGGCCTTGAACACAGGCCGAACCTGAGGGCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTCTTACTCAGGAATCTGTGTGCC  
 CAACCCATGGACAGGCCACGCTGGGGCCACATGCTGACACAGCTCATCAGAGACCCCTTA  
 GACACTGACAGGCCCTCTCTCAGCCCTTCTCTTTGTCAGAGATTCCAAGCTGGATAAGTT  
 GGTCAATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 54**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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REQGRGIHVIVLNQATGHVMAKRVFDITYSPHEDEAMVLFLLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDWTAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKPPSVTPIFLEPPPKKEGAPGAPEQT
```

**Important features of the protein:****Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGAACCAACACAC  
 CTGTTTAAAGAACTAAGCACCATTAAAGCCCACTGGAAATTTGTTGCTAGTGGTTTGGGGTGAATA  
 AAGGAGGGCGAATGGATGATTTTCATCTCCATTAGCCTGCTGCTCTGGCTATGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTCCTCTGGCTGTTAATTTCTCAGAGGAACGACATGAAGCTGGTGACATGTTTTGG  
 GTGCTGGCCTTCTCTGTTGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA  
 GATATCTTGGAGGAAAACACCAAGCAAGTGAACACATAATGTGATTGTCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCAGCACACACAGCTGCATGCCATATTTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACGAGATTGGTAACTCCCATGTGCATTTCT  
 ACTGACGATCCAGAAGCAGCAAGGCTAGCAATTCAAAAATCACCACCACGCTGGGTCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCAACAGCCAGTGTCCAGTTAATTG  
 TGTGTTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCCTTCTTGATGCTATGCT  
 GGCCTAGAGCGGAATCGAATCAGAAAGCACTTGTGGTCTTTGCAATTTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAACCCCTTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGA  
 ATAGGGCAGACGCAAGCCGATGCCACGGGAGGGAGAGGCTCAGCCGCTGGAAAGTGGCAGCCCT  
 GGTTCCTGGGTGCTCATCCCTCTCATCTCTGTCAGTAGGACACCAGCATTAATGTTTCAAGGTCCAGC  
 CTTGGCTCAGGGCCGTTTGGCATCCAGTGAGAACAGCCGGCAGGTGACAGCTACTCACTTCCCTCAGTC  
 TCTTGCTCAGCTTGGCCTCTCATAGTATTTCTAGAGTCAGAGGGGAGGTGAGGTTAAACCTTG  
 AGTAATGGAAAAGCTTTTAGAGTAGAAAAACATTTACGTTGCAAGTTAGCTATAGACATCCCATTTGTGT  
 TATCTTTTAAAGGCCCTTGACATTTGCGTTTAAATATTTCTTAAACCTATTCTCAGGGAAGATG  
 GAATTTAGTTTAAAGAAAGAGGAGAACTTCATACTCACAATGAAATAGTATTATGAAATACAGT  
 GTTCTGTAATTAAGCTATGTCTCTTCTCTTAGTTTAGAGGCTGTGACTTTTATCCATTGATTTTT  
 AACATGTTTCCACCATTGTAAGACTGGTGTCTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA  
 GCACCCACTCACTTAGATGCTAAAGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC  
 AAGACACATTGAAAGCTCTCTTTATATCAAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT  
 TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAAAT  
 ACCTGTCTCCACATTCCTAGAGAGGAGCCAACTTCTAGTAGTTTCAGTTCTAGGCTTCTCTCAAGAA  
 CAGTCAGATCACAAAGTGTCTTTGGAATTAAGGGATATTAATTTAAGTGATTTTGGATGGTTAT  
 TGATATCTTTGTAGTAGCTTTTTTAAAGAGCTACCAAATGATGGTGTGCCCTTTTTTTTGTGTTTT  
 TTTTTTTTTAATTTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAGCTTT  
 GGCAGACTGTGCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTCGCCTA  
 TTGATTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGCTCTTTCTTGTCTTTCTCTCAACTTT  
 TCCCTCTAGCCCTCTCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATT  
 CTTTACAGGACAACCACTTCTCGAACTGTAATAATGAAGATAAATAATCTTTATCTTTATCCCTTT  
 CAAAGAAATFACCTTTGTGTCATAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCTCATGTGTAA  
 ATTGACCAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA  
 ATTTTTTTTTCATATTTTGCCAAAATTTTGTAAACCCGTCTTGTCAAAATAGTGATATATATTTGAT  
 TATTAATTTATTTTACTTTCTATACCAATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGAGCTAGTAGTTTGTAAAAACGTTTCTATGACGCATAAGCTAGCATGCCATGATG  
 ATTTATTTCTTCTCAATGTTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTCTGCT  
 GGCCACAGTGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCACTGGCAACAATTTGCATACA  
 ATTTTACTACCAAGAGAAGTATAGTATGGAAGTCCAAATGACTTCTGTGATGGATGTACAGCT  
 GACTGGGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACATATATGGTTGCCTAGATTCTCTCTGGA  
 AACTGACTTTGTCAAATAATAGCAGATTGTAGTGTCAAAAAA

**FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLILSVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304



**FIGURE 57**

GCTCGAGGCCGGCGCGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGACATGATGGGCTTGG  
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCGGCCCTGGTGCCCTGCATC  
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA  
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA  
 TAACATCACCCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCTGCAGA  
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
 GCAGCAGGCCTGCCACACAGAGGTGCCACAAGGAAGGGAACGTGCTTGGTAACAGCAA  
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
 CCAGGCCGGGAGCAGGTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
 GCCGGGGAAGGGAGAAAACAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAACTCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
 AATCATACACTCTGAATTGAACTGGAATCACATATTTCAACAACAGGGCCGAAGAGATGACTA  
 TAAAAATGTTATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

**FIGURE 58**

MMGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFOLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLLQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQLQALSEFPRLQAAGLPHTTEVPQKGKGNVLGNSKSQTPAPSSEVVLDSCR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

2003-2004-2005-2006-2007-2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025-2026-2027-2028-2029-2030-2031-2032-2033-2034-2035-2036-2037-2038-2039-2040-2041-2042-2043-2044-2045-2046-2047-2048-2049-2050-2051-2052-2053-2054-2055-2056-2057-2058-2059-2060-2061-2062-2063-2064-2065-2066-2067-2068-2069-2070-2071-2072-2073-2074-2075-2076-2077-2078-2079-2080-2081-2082-2083-2084-2085-2086-2087-2088-2089-2090-2091-2092-2093-2094-2095-2096-2097-2098-2099-2100-2101-2102-2103-2104-2105-2106-2107-2108-2109-2110-2111-2112-2113-2114-2115-2116-2117-2118-2119-2120-2121-2122-2123-2124-2125-2126-2127-2128-2129-2130-2131-2132-2133-2134-2135-2136-2137-2138-2139-2140-2141-2142-2143-2144-2145-2146-2147-2148-2149-2150-2151-2152-2153-2154-2155-2156-2157-2158-2159-2160-2161-2162-2163-2164-2165-2166-2167-2168-2169-2170-2171-2172-2173-2174-2175-2176-2177-2178-2179-2180-2181-2182-2183-2184-2185-2186-2187-2188-2189-2190-2191-2192-2193-2194-2195-2196-2197-2198-2199-2200-2201-2202-2203-2204-2205-2206-2207-2208-2209-2210-2211-2212-2213-2214-2215-2216-2217-2218-2219-2220-2221-2222-2223-2224-2225-2226-2227-2228-2229-2230-2231-2232-2233-2234-2235-2236-2237-2238-2239-2240-2241-2242-2243-2244-2245-2246-2247-2248-2249-2250-2251-2252-2253-2254-2255-2256-2257-2258-2259-2260-2261-2262-2263-2264-2265-2266-2267-2268-2269-2270-2271-2272-2273-2274-2275-2276-2277-2278-2279-2280-2281-2282-2283-2284-2285-2286-2287-2288-2289-2290-2291-2292-2293-2294-2295-2296-2297-2298-2299-2300-2301-2302-2303-2304-2305-2306-2307-2308-2309-2310-2311-2312-2313-2314-2315-2316-2317-2318-2319-2320-2321-2322-2323-2324-2325-2326-2327-2328-2329-2330-2331-2332-2333-2334-2335-2336-2337-2338-2339-2340-2341-2342-2343-2344-2345-2346-2347-2348-2349-2350-2351-2352-2353-2354-2355-2356-2357-2358-2359-2360-2361-2362-2363-2364-2365-2366-2367-2368-2369-2370-2371-2372-2373-2374-2375-2376-2377-2378-2379-2380-2381-2382-2383-2384-2385-2386-2387-2388-2389-2390-2391-2392-2393-2394-2395-2396-2397-2398-2399-2400-2401-2402-2403-2404-2405-2406-2407-2408-2409-2410-2411-2412-2413-2414-2415-2416-2417-2418-2419-2420-2421-2422-2423-2424-2425-2426-2427-2428-2429-2430-2431-2432-2433-2434-2435-2436-2437-2438-2439-2440-2441-2442-2443-2444-2445-2446-2447-2448-2449-2450-2451-2452-2453-2454-2455-2456-2457-2458-2459-2460-2461-2462-2463-2464-2465-2466-2467-2468-2469-2470-2471-2472-2473-2474-2475-2476-2477-2478-2479-2480-2481-2482-2483-2484-2485-2486-2487-2488-2489-2490-2491-2492-2493-2494-2495-2496-2497-2498-2499-2500-2501-2502-2503-2504-2505-2506-2507-2508-2509-2510-2511-2512-2513-2514-2515-2516-2517-2518-2519-2520-2521-2522-2523-2524-2525-2526-2527-2528-2529-2530-2531-2532-2533-2534-2535-2536-2537-2538-2539-2540-2541-2542-2543-2544-2545-2546-2547-2548-2549-2550-2551-2552-2553-2554-2555-2556-2557-2558-2559-2560-2561-2562-2563-2564-2565-2566-2567-2568-2569-2570-2571-2572-2573-2574-2575-2576-2577-2578-2579-2580-2581-2582-2583-2584-2585-2586-2587-2588-2589-2590-2591-2592-2593-2594-2595-2596-2597-2598-2599-2600-2601-2602-2603-2604-2605-2606-2607-2608-2609-2610-2611-2612-2613-2614-2615-2616-2617-2618-2619-2620-2621-2622-2623-2624-2625-2626-2627-2628-2629-2630-2631-2632-2633-2634-2635-2636-2637-2638-2639-2640-2641-2642-2643-2644-2645-2646-2647-2648-2649-2650-2651-2652-2653-2654-2655-2656-2657-2658-2659-2660-2661-2662-2663-2664-2665-2666-2667-2668-2669-2670-2671-2672-2673-2674-2675-2676-2677-2678-2679-2680-2681-2682-2683-2684-2685-2686-2687-2688-2689-2690-2691-2692-2693-2694-2695-2696-2697-2698-2699-2700-2701-2702-2703-2704-2705-2706-2707-2708-2709-2710-2711-2712-2713-2714-2715-2716-2717-2718-2719-2720-2721-2722-2723-2724-2725-2726-2727-2728-2729-2730-2731-2732-2733-2734-2735-2736-2737-2738-2739-2740-2741-2742-2743-2744-2745-2746-2747-2748-2749-2750-2751-2752-2753-2754-2755-2756-2757-2758-2759-2760-2761-2762-2763-2764-2765-2766-2767-2768-2769-2770-2771-2772-2773-2774-2775-2776-2777-2778-2779-2780-2781-2782-2783-2784-2785-2786-2787-2788-2789-2790-2791-2792-2793-2794-2795-2796-2797-2798-2799-2800-2801-2802-2803-2804-2805-2806-2807-2808-2809-2810-2811-2812-2813-2814-2815-2816-2817-2818-2819-2820-2821-2822-2823-2824-2825-2826-2827-2828-2829-2830-2831-2832-2833-2834-2835-2836-2837-2838-2839-2840-2841-2842-2843-2844-2845-2846-2847-2848-2849-2850-2851-2852-2853-2854-2855-2856-2857-2858-2859-2860-2861-2862-2863-2864-2865-2866-2867-2868-2869-2870-2871-2872-2873-2874-2875-2876-2877-2878-2879-2880-2881-2882-2883-2884-2885-2886-2887-2888-2889-2890-2891-2892-2893-2894-2895-2896-2897-2898-2899-2900-2901-2902-2903-2904-2905-2906-2907-2908-2909-2910-2911-2912-2913-2914-2915-2916-2917-2918-2919-2920-2921-2922-2923-2924-2925-2926-2927-2928-2929-2930-2931-2932-2933-2934-2935-2936-2937-2938-2939-2940-2941-2942-2943-2944-2945-2946-2947-2948-2949-2950-2951-2952-2953-2954-2955-2956-2957-2958-2959-2960-2961-2962-2963-2964-2965-2966-2967-2968-2969-2970-2971-2972-2973-2974-2975-2976-2977-2978-2979-2980-2981-2982-2983-2984-2985-2986-2987-2988-2989-2990-2991-2992-2993-2994-2995-2996-2997-2998-2999-3000

**FIGURE 59**

GGATG CAGAAAGCCTCAGTGTTCCTGCTCTTCTGGCCTGGGCTGCTCTTCTCTTCTACGCTGGCATTGCCCTCTTCA  
 CCAGTGGCTTCTGCTCACCCGTTTGGAGCTCACCACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC  
 TGCCATGGGGAGCCAAAGGAAACCTGGGGCTGCTGGATGCTTCCGATTTTCGGGGTTGTTGGTGTCTGA  
 TAGATGCTCTGCGATTGACTTTCGCCAGCCCCAGCATTACACGTGCTTAGAGAGCCCTCTGTCTCCCTACCCT  
 TCTCTGGGCAAACTAAGCTCCTTGAGAGGATCCTGGAGATTGAGCCCAACCATGCCGGCTCTACCGATCTCAGG  
 TTGACCCCTTACCACCACCATGAGCGCCTCAAGGCCCTCACCCTGGCTCTGCTACCTTATTATGATGCTG  
 GTAGTAACCTTCGCCAGCCACGCCATAGTGGAAAGACAATCTCATTAAGCAGCTCACCAGTGAGGAAAGGGCTGAG  
 TCTTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTCCCATCTTGA  
 ATGTCAGAGACCTAGACAGCTGAGCAATGGCATCCTGGAAACACCTTACCCACCATTGGACAGCTGGTGAATGGG  
 ACGTGTCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGCCA  
 AGAAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCGCTGGAGAAATGACACACTGCTGGTAGTGG  
 CTGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGTGAGTGGAGTCTCAGCTGCTCTCTTTC  
 TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCCTTGTGC  
 CCACGCTGGCCCTGCTGCTGGGCTGCCATCCCATTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG  
 GGGGTGAGGACTCCAGCCCCACTCCTCTGCTTTAGCCCCAAGCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT  
 CCGAATTTCTCATACTACTCAGCTGTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT  
 TCTCCAAAGCCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCACTGTGA  
 TTGCTGAGCTGCAGCAAGTTCCTCGGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC  
 GCATGGCGGGGGTACTGCTCTCTGGCTGCTTCTGCTTTATCTGCTGCTGGCATCTCAGTGGGCAATATCCC  
 CAGGCTTTCCATTTCGCCCTCTACTCTGACACTGTGSCCTGGGGCTGGTTGGGGCCATAGCGATGCTGGAC  
 TCTCGGGAATATTGAGCTGAAGCTAGATCTAGTGTCTTAGGGGCTGTGGCTGAGTGGAGCTCATCTCTCCCTT  
 TTCTGTGGAAGCTCCTGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCTGTTTCCGCTCCTCGGCCGCTCC  
 TGTACTCTCTGCTGCTTTTCGCTGGCTGTGTTCTCTCTGATAGTTTGTGTGAGCTGAGGCCAGGGCCACCCCT  
 TCTTTTGGGCTGATTCTGCTGCTCTGCTGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACTTAAGCTAC  
 TCACAATGCCCGCCTTGGCACTTCAGCCACAACAAACCCCCAGGCCACAATGTTGATATGCCCTGAGGCTTG  
 GAATTGGTGTCTTTTATAGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACTGTTTGGCACT  
 CCTCTCCTGGCTGAGTCTCTGTGCATCCATGGTGGTGGTGGAGCCAAAGAAATTTATGGTATGGAGCTTGTGTGG  
 CGGCGCTGTGGCCCTGTTAGCTGCCGTGCCCTTGTGGCTTCGCCGTATGGTAATCTCAAGAGCCCCAGGCCAC  
 CCATGCTCTTTGTGGCTGGGAGTGCCTAATGGCAATGGGTACTGCTGCCCTACTGGGCATTGGCGTGGGGG  
 CAGATGAGGCTCCCCCGCTCTCCGGGTCTGGTCTCTGGGGCATCCATGGTGCTGCCCTGGGCTGTAGCAGGGC  
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA  
 GGACAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGTCCTCCAA  
 TCTACCGACACATGCAGGAGGAGTTCGGGGCCGGTTAGAGAGGACCAAAATCTCAGGGTCCCCTGACTGTGGCTG  
 CTTTACTAGTTGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCTGTTGGGCTTCCACTTCTGCTGT  
 TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTCCTGCAGAGCTTCTTCTCTACATCTGCTTGTCTG  
 CTGGGATACCGCTCACCACCTGGTCTTTTACTGTGCCATGGCAGGCACTCGGCTGGGCCCTCATGGCCA  
 CACAGACCTTCTACTCCACAGGCCACCAAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATCCC  
 CAGAGGGTCATGGCTCCTGTACTTGGCTGCTGCTTTGCTAGTGGGAGCCAACACCTTTGCTCCCAACCTCCTCT  
 TTGAGCTAGGTGCCACTGCTCTGCTCTGGCTTTCTCTGTGTGAGAGTCAAGGGCTGCGGGAAGACAGCAGCG  
 CCCCAGGAAATGAAGCTGATGCCAGATCAGACCCGAGGAGGAAGGAGCCACTGATGGAGATCGCGCTCCGGC  
 ATGCGCTCAGCATTCTATGCAGCACTGCTGCAGCTGGGCCCTCAAGTACCTCTTATCCTTGGTATTCAGATTCT  
 TGCTGTGGCTTGGCAGCTCCATCCTTCGAGGCACTCATGGTCTGGAGTGTGGCCCTAAGTTTCATAT  
 TTGAGCTGTGGCTTTCATTGTGAGCAGCGTGGGACTTCTCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG  
 CTGTGAGCTGTGAGGAGTATTTCTGGGCCAGCAGGAGTGGCTGATCTGTGATGCTGATGCTGAGCTTGGCT  
 ACAGAGAGTGCTGGAGAACAGTGTAGCTTGGCCTGTACAGTACTGGATGATCTCAAGACAGGCTCAGCCATAC  
 TCTTACTACTATGCAGCAGGGGCCGCTGACATCTAGGACTCTATTATTTCTATAATCAGGACCACTGGAGTGA  
 TGTATCCTTAACCTCTGATTTGGATGCACTGAGGGAACAGGGGGCGCTGCCAAGTGAATAAATGAGCCCG  
 CGCTGTGACTTGCACCTAATGCAGCACTTGGGAGGACAGGTGGAGAGTTCTTGGTCCAGGAGTCTCA  
 AGACCAGCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAAAGTGAATAAATGATAATAT

**FIGURE 60**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQKPGACW
MASRFSRVVLVIDALRFDFAPQHQSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTTMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVRVFMGDDTWKDLF
PGAFSKAFFFPFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGHHPHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAAFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAEFLSGGEDSQPHSSALAQASALHLNAQ
QVSRLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAIISPGFPFCPLLLTPVWGLVGAIA
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLA
VFFSDSFVVAEARATPFLLGSFILLVVLHWEQGQLLPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRLVLSGASMLVP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLFLQSFLL
LLHLLAAGIPVTTGPFPTVPWQAVSAWALMATQTFYSTGHQPVFFAIHWHAAVFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEP
LMEMLRLDAPQHFYAALLQLGLKYLFIHQIILACALAASILRRHLMVWKVFAPKFI FEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT  
 GTCTCTGGTGGTTTGCCATAAACCTGCAAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
 CCTGACAGCTCCAGAGAAGTGGAAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGCTGTGTTGAATACATAATCAACAGAACGTGGTCC  
 CAGTGTGTGACCAACACACGCTGGTGTCACTGGCTGGAGCCGAACACTCTTTACTGCGT  
 ACACGTGGAGTCCTTCGTCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTG  
 CCCATATCTATTACCGTGTTCCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTATGGAATGAATTTGACAAAA  
 GATTCTTTGTGCCTGCTGAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT  
 TCTAAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
 GGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAAACAGTCATTGAATATGA  
 ATATGATGTCAGAACCCTGACATTTGTGCGGGGCCGAAGAGCAGGAGCTCAGTTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATGGAGTCGAGGCAGCGTTGGCAGTCTTGGGCCCCG  
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCTGGTCGACTGGGATCCCC  
 AAAGTGGCAGGCTGTGTATTCTTCGCTGTGTCAGCTTCGACCAGGATTCAGAGGGCTGCGAG  
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTATGAGGAGGAATGGGGGT  
 TATATGTGCAGATGAAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAA  
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT  
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTATTCTCATAGCAGTGTGTGATTG  
 GTTCATGCTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGT  
 GTTCTATGCAGAGAAAGCAGTCAATAAATGTTGCCAGACTGGGTGCAGAAATTTATTTCAGG  
 TGGGTGT

**FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815  
<subunit 1 of 1, 442 aa, 1 stop  
<MW: 49932, pI: 4.55, NX(S/T): 5  
MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIIHVGKEKH PANLILYGNF D  
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVRTTDICAGPEEQELSL  
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLDP LAQEHTDSEEGPEEE PSTTLVDWD  
PQTGRLCIPSLSSFDQDSEGCEPSEG DGLGEEGLLSRLYE EPAPDRPPGENETYLMQFMEEW  
GLYVQ MEN

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCGCAGCCTGCG  
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCTT  
GATGCTGCCCGTGAAGCCCCCGCAGGCTCTGGGGGGCCAGATCATCGGGGGCCACGAGG  
TGACCCCCACTCTCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCGAGCCCGTGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGBCCTGCTGCTGGGCGCCACGTCTGAGTACTGCGGAGCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTACCACGCACCCGACTACACCCCATGACCCACGCCAACAGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTCGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAAGGGCCAGGCCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGCTCTGACTTTGAGGAGCTGCCGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC  
CCGGACGTCTGCAACAGCTCTTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGAGAGGGCCCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCCTCGTTTCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC  
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTGCGCGGAGCAGTCC  
TCAGCCCGGCCCCCTGACCTGGGACCAACAGGCCCCCAAGGAGAACCGCCCT**TGAG**GCCCAACT  
TGGGCGATGCAATGAGATGGCGCGCTCAGGCCCTGGAATGTTCCTGGCTGGGCCCCACGGG  
AAGCGTGATGTTAGGTTGGGGTGGGACGGGACGCGTGGGCGCACCCATTCCACATGCA  
AAGGGCAGAAGCAAAACCCAGTAAATGTTAACTGACAAAAAAGAGAAA

100306

100306

100306

100306



**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
 CGCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGTGCGCGCTGTGCGCGCTGGGCACGGTAG  
 CAGGCGCCGCGCTGTGCTCAAGGACTATGTCAACGGTGGGGCTTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTCTCTTGACAAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT  
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT  
 TCCGGAAGTACTTTCGATGGACTCAAACAGAAGGCCCGGCCCGGAGGCTGAGGATGAGGA  
 GGTGGCCCGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
 GGGAGCAGCCCCCTCCCCAGATAACTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGTCCGCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG  
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGC  
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
 TGTGCACCTGTCAGGCCACGTGAGGAGAGCCAGCGGTGCTGTCGGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
 TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAATGCTCAGAATAACTG  
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
 GGTGTTTGTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCTATCCC  
 GAGTTCAAGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA  
 TTGCTGGGACTCCCACCTTCCCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAC  
 TTGCTCATTT

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842  
><subunit 1 of 1, 331 aa, 1 stop  
><MW: 35932, pI: 8.45, NX(S/T): 1  
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG  
GNIILACRDMEKCEAAAKDIRGETLNHHVNRHLDLASLKSIREFAAKIIEEEERV DILINN  
AGVMRCPHWTTEDGFEMQFGVNLGHFLLTNLLLDKLGASAPSRIINLSSLAHVAGHIDFDD  
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF  
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW  
AESARLVGLEAPSVREQPLPR

**Signal peptide:**

amino acids 1-17

1007306123107

**FIGURE 67**

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
 CAGCGTGGCGCGCGCCCTGGCGCCGAGCGCCGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGTCAT  
 GAGGATTCACAAACCCCTGTGGCTAACCTCTGCTTGCATTTACTCTCATCAAACGCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA  
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
 ATTCCATGGCTGGAGGAGGTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGACAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC  
 TGAGGCTGTCTCCAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTCAGACCTGGGTTCCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCTTAT  
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCCACCTGGA  
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGCCATCAGGGGAGAAGCAAGTTACAAGTGGAG  
 TACCGCATCAGCAAAAGTGCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCCTCAA  
 CCACCGCATTTGCTGCCCTCAGGCGCTTGATGTCCGGGCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCAACCAAGC  
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGGTGGAACTGCAAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCCCTGTCTGGTGGGAGATAAGTGGGTGGCCAAACAAGTGGATACATGAGTATGG  
 ACAGGAATTCGCGAGACCTGTCAGCTCCAGCCTGAAGCA**TGA**ACTGTTGGCAGAGAGAAGC  
 TGGTGGAGTCTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCCCTCGCAATCAGAGGC  
 AAGGGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
 GTCAGAGTAGGATGTCACAGTACAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG  
 AGTTCAGTACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTCCATCAGTGGGTC  
 TTTTGGCACTTTGAACCTTGACCACAGGACCAAGAAGTGGCAATGAGGACACTGCGAGAG  
 GGGCTAGCCTGACTCCAGAACTTAAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCAAG  
 CAGGAGTGTCCCCCTCCCAAGCATATCCAGATGAGTGGTACTATATAGAAGATTTT  
 TTTAAGTTGAAAACACTTTCTTTTCTTTTGTATGATGGTTTTTAAACAGTCATTA  
 ATGTTTATAAATCAAAA

**FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSSVARALAPERRLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLSEASINIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTVTSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAI PWLEEAVSLFRGSYGWKTEDASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19

10017306123001

**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCTGCTCCCACCCCTAG  
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCGAGCCCCGTAACCCGCGCGGGGAG  
 CGCCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
 TGGCTCAAGTTTTACATTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT  
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCCTCC  
 TGGCTCCAGCCATCATCTCATCCTCCTGGGCGTCGTCATGTTATGGTCTCCTTCATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT  
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
 ACTTCTGAAACGACAACATTGGAAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
 AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGTGCCCCACA  
 CCTGTGTCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC  
 AAGGAGCGTTTCAGTGTGCAGGATGTATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
 CTGGTTCATGGACAACATACCCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG  
 ATGCTGCTTGTGCTACCCCAATAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA  
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCGCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
 CCCAGGGAGCAGAGCTGGGCCTCCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT  
 GCCACCTGGGGCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
 GAGCTGAGGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA  
 GGCAGTTTTGTAGCACTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG  
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGC  
 CTCTTCTCAGCCTCCCAGGTGCCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA  
 GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAACCAAGTTTGTAA  
 TCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAA

### FIGURE 70

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIIYAEVERQKYKTLES AFLAP
AIIILLGVVMFMVSVFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGIE NYDDDLDFKNIMDFVQKKFKCCGEDYRDVNIWIFQHDSCAPGFLACGVPTCC
IRLNTVEVNTMCKGYKTIKERSFVQDVIIYRGCTNAVIIWFMQNDYTIMACILLGILLPQFLG
LITLLTYITRVEDIIEMHSFTDGLLGPAGKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGA  
 CACCTGGGAAG**AATG**CGCCGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGTGGCAGCCACC  
 TTGATCCAAGCCACCCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCCATGCGGGAAAAGCCAGCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
 GTCCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCACATGACGACTGAGGCCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC  
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACAGCTGTGTCCCGTG  
 ATCGAGGCTTCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTTC  
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTC  
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCTGTGG  
 ACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCACTGATCGTGTGGAAGTGTTCCTCCCA  
 GTGAAGCCCTCCGCCCTTGTTCACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC  
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCCATCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCAGTGTCAATTGGTG  
 AAGGCCTTGGGATTCGAGGACAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  
 AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAG**TGA**AGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGGTCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
 CAATAAACACTTGCCTGTGAAAAA

**FIGURE 72**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881  
><subunit 1 of 1, 484 aa, 1 stop  
><MW: 52468, pI: 7.14, NX(S/T): 3  
MAGPWTF<sup>1</sup>TL<sup>2</sup>LCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSI<sup>3</sup>LQQLPLLSAM  
REKPAGGIPVLGSLVNTVLKHHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL  
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN  
LLVPSLPLNLVKNQ<sup>4</sup>LC<sup>5</sup>PVIEAS<sup>6</sup>FNGMYADLLQLVKVPISLSIDRLEFDLLYP<sup>7</sup>AIK<sup>8</sup>GDTIQLYL  
GAKLLDSQ<sup>9</sup>GKVTKWFNNSAASLT<sup>10</sup>MPTLDNI<sup>11</sup>PFSLIVSQDVVKA<sup>12</sup>AAVA<sup>13</sup>AVLSPEEFMVLLDSVL  
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSS<sup>14</sup>SEAL  
RPLFTLGIEASSEAQFYTKG<sup>15</sup>QDLILNLN<sup>16</sup>NISSDRIQLMNSGIGWFQPDVLKNIITEI<sup>17</sup>HSIL  
LPNQNGKLRSGVPVSLVKALGF<sup>18</sup>EAAESSLT<sup>19</sup>KDALVLT<sup>20</sup>PASLWKPSSPVSQ

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457



**FIGURE 73**

GAGCGAACATGCGAGCGCTTGGCGGTTTTGGTGTGCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAGGAGATGGTGTATCTGA  
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTATCGTCATGTTCACTGCT  
 CTCCAACTGTCATAGACAGTGTGTCGTTTGCAGCAAGCTGATGAAGAATCCAGATCCTGGC  
 AAACCTCTGGCGATACCTCCAGTGCATTACCAACAGGATATTTTTGCCATGGTGGATTTTG  
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTTCAGCTCCAACTTTTCATCAACTTT  
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC  
 TGAGCAGATTGCCCGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCTTTATGTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
 CTTTGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTCAGCTTTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA  
 GCTGAAACACACATTGTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTATTTCTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTTCGATGAGTTAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC  
 CTCTTTTTTTCAGTGATTTAAATAGTTAATCATTTAAACCAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTGAAAATAAATTATCCTTTAACCTTCTCTT  
 CCCAGTGAACCTTTATGGAACATTTAATTAGTACAAATTAAGTATATTAAAAAATTGTAAAA  
 CTACTACTTTGTTTTAGTTAGAACAAGCTCAAACTACTTTAGTTAACTTGGTCACTCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGGAAGTAAGTCTGACCAGGTGTTCCACATATGCC  
 TGTTCAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTATGTGTCTCATGTGGTCTTCTGAAAATG  
 GAACACCATTCTCAGAGCACGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
 GCATATTTCCCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCTCTAAATACAGGATTATAAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTAGAAA  
 GATTTTCAGATTCATTCCATCTCCTTAGTTTTCTTTAAAGGTGACCCATCTGTGATAAAAAATA  
 TAGCTTAGTGCTAAAACTAGTGTAACCTTATACATGGCCTAAAAATGTTTCTACAAATTAGAGT  
 TTGTCACTTATTCATTGTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTTACCGCTGTAATCTCAGCACTTTGGGAGGCCAAGCGAGGCAGATCAC  
 GAGGTTCAGGAGTTTCGAGACCATCTTGCCCAACATGGTGAACCCCGTCTCTACTAAAAATAT  
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

1007306 303104  
 1007306 303104

**FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTNKRPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFINFPKAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSI FRSKYHGYPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

100173062301

**FIGURE 75**

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTTCGCTGTCCCTGCCCTGCTCTGCTAGGGAGA  
 GAACGCCAGAGGGAGGCGGCTGGCCCCGGCGGAGGCTCTCAGAACCGTACCGGGC**ATG**CTA  
 CTGCTGTGGGTGTCGGTGGTGCAGCCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA  
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGGTCTGTGAGCGACTCCTTCGATG  
 GAAGGTTAACATTTTCATCCAGGAAGTCAGGTAGTGAACCTCCCTTTTATCAACTTTATGAAG  
 ACAGTGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGC  
 AGCAATGTGGAGTGGCCTCTTCACTCACCTAACAGAATCTTGGATAATTTTAAAGGCTCTAG  
 ATCCAAATTTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT  
 GGGAAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG  
 AGATGTTGCTTTCTTACTCAGACAGAAGGCGAGGCCCATGGTTAATCTTATCCGTAACAGGA  
 CTAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAACCTGGTTAAGA  
 AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAAATTTACCACACCC  
 TTACCTTTCAACATCTCTCGAGAAAAATTTGGATCTTCAACATTTACACATCTCTTTATTT  
 GGCTTGAAAAAGTGTCATGATGCCATCAAAATCCAAAGTGGTCACCTTTGTGAGAAATG  
 CACCTGTAGATTATTACTCTCTTATACAAAAAAGTGCCTGGAAGATTTACAAAAAAGA  
 AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG  
 AAATTAATTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTATTGTCATATACCTCTCA  
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG  
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCGGCTACAAGTATCAAAATG  
 TGGTTTCTCTTGGGATATTTACCTACCATGCTTGATATTTGCTGGAATTCCTCTGCCTCAG  
 AACCTGAGTGGATACTCTTTGTTGCCGTTATCATCAGAAACATTTAAGAAATGAACATAAAGT  
 CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA  
 CCTACATGCTTCGAACTAACCACTGGAATATATAGCCTATTCGATGGTGCATCAATATTG  
 CCTCAACTCTTTGATCTTTCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAAATTTCC  
 AGAAATTACTTATTTCTTTGGATCAGAAGCTTCATTCATTATAAACTACCCCTAAAGTTTCTG  
 CTCTGTGCCACCAAGTATAATAAAGAGCAGTTTTATCAAGTGGAAACAAAGTATAGGACAGAAT  
 TATTCAAACGTTATAGCAAACTTTAGGTGGCACCAGACTGGCAGAGGAACCAAGGAAGTA  
 TGAAGATGCAATTGATCAGTGGCTTAAACCCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAA  
 GTTTAAAAATAGTGTTCTAGAGATACATATAAATATATTAAGAATCATAATTATGATTTT  
 AAATGAAACAGTTTTAATAATTACCAAGTTTGGCCGGGCACAGTGGCTCACACCTGTAATC  
 CCAGGACTTTGGGAGGCTGAGGAAGCAGATCACAAGGTCAAGAGATTGAGACCATCTCTGC  
 CAACATGGTGAACCCCTGCTCTACTAAAAATACAAAAATAGCTGGGCGCGGTGGTGACA  
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG  
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCTGGCAACAGAGTGAGACTGTGTCCG  
 AAAAAATAAAAATAAATAATAATAATTACCAATTTTCCATTTTGTAAAGATGTAGTG  
 TATTTTAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAATGGTTATTATTTA  
 GGCCTTTGTACAATTTCTAACAAATTTAGTGGAAGTATCAAAAGGATTGAAGCAAACTACTGTA  
 ACAGTTATGTTCTTTAAATTAATAGAGAAATATAAAATATTGTAATAATATGTATCATAAAT  
 AGTTGTATGTGAGCATTTGATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 76**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHFGSQVVKLPFFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGVRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVMNLI RNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMPGPIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGYSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

```

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

**FIGURE 77**

GAGAGAAGTCAAGCTGAGAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG  
GCCTCTCTTGGCCTCAAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
GGTGGCCATGCTGCTCCCAAGCTGGAAAACAAGTTCATTATGTGCGTGCCAGCATTGTGACAG  
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATACCCCA  
TGTGACATCTATAGCACCTTCTGGGCTGCCCCTGACATCCAGGCTGCCAGGCCATGAT  
GGTGACATCCAGTGCAATCTCCTCCTGGCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
CAGTCTTCTGCCAGGAATCCCAGGCCAAGACAGAGTGGCGTAGCAGGTGGAGTCTTTTTC  
ATCCTTGGAGGCCTCTGGGATTCACTCTGTTGCCCTGGAATCTTACATGGGATCTACGGGA  
CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC  
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
ATGTGTCAAGAAACAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
CACCCCGAGGGCCACAGGTGAGGGGACACTACCACTGGATCGTGTCAGAGGTGCTGCTGAGG  
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG  
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCTCACCTTGCTGCTC  
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGG  
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAACCCACTAATCACATCCCACTG  
ACTGACCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCACCTTGTGTTATGACTCCACAGTGTC  
AGACTAATTTGTGCTGAAGTCAACTGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAG  
GATGCAGGATGGGAGGACAGGAAGGCAGCTGGGACATTTAAAAAATA

**FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886  
><subunit 1 of 1, 230 aa, 1 stop  
><MW: 24549, pI: 8.56, NX(S/T): 1  
MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVF  
FILGGLLGFIPIVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS  
SQRNRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGIV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**FMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC  
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG  
TGAAGCTGAAGGTCAGGGTGTGAATCCCACTGCCACTCATCTCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCCCTTGAGAGACATAGAAAGAAAATCAACTTCTACTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCACTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

**FIGURE 80**

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPA PRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTND FVVKLVQGVNSQCHSSPIS SKCESRRRFP

**Signal peptide:**

amino acids 1-25

1001 206 123101  
10121 902 1001



**FIGURE 81**

CTCCACTGCAACCACCCAGAGCC**ATG**GGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCA**GA**TTGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGGAACCCCTCACCCCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

**FIGURE 82**

MAPRGCIVAVFAIFCISRLLCSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDsARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

1007306123101

**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGACGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCCGCGCGCTCCCGCCCGCTCCCGGCACAGAAAGTTCCCTCT  
 GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGGTGCG  
 CACGCCGTATTCCCTGTATGTCTGTCCGAGGGGCAGAACGTACCCCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCAGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GCGAGGTGCAGACCTGCTCAGAGCGCCGGCCATCCGCAACCTCACGTTCCAGGACCTTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACCTCGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAGATGCACCATCCAACCTGTGTGGTGT  
 ACCCATCTCTCTCCAGGATAGTGAAACATCAGGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACCGCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAC  
 CGGGCTTTGAAGCCTCACCACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG  
 TCCATGTGTGGCCAGCGGCAGCCTTCTGAGTCTGGCGGCATCTGCTTTCGGAGCCACGAC  
 CCCCCTGTCTCCTCCAGGCCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT  
 CTCCAACCTTTGAGGTCATCTAGCCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCCTCGGCCCTGGTTC  
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAAGCCAGCCCTCAACCCCTC  
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGTGCTGAG  
 ATTCTCCCTAGAGACCTGAAATTACACAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCAGGTG  
 GAGAGACTTCTCCCCGTGGCCGCCTTGGCTCCCCGTTTGGCCGAGGCTGCTCTTCTGTC  
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCACATGGCCATCGCC  
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGGTGGGTGGGCTTCTGGGAAGGTGA  
 GTGGAGAGGGGACCTGCCCCCGCCCTCCCATCCCTACTCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAACTACATGGGGAAAAA

**FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897  
><subunit 1 of 1, 311 aa, 1 stop  
><MW: 33908, pI: 6.87, NX(S/T): 6  
MGVPTALEAGSWRWGSLFLFALFLAASLGPVAAFVATPYSLYVCPEGQNVTLTCRLLGPVVK  
GHDVTFYKWTYRSSRGVEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVVPSSSQ  
DSENITAAALATGACIVGILCLPLILLLVYKQQAASNRRQAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

**FIGURE 85**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
 TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTCCACCTTAGACCTCCCTTCTGCCCCC  
 TTTCTGCCCCACCGTGCTTCTGCCCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTTGATCTGTGGCCCCGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCCCGA  
 CTCGCTCCCGGACCAGCGGCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGTCCTC  
 TCCTCCTTGTGCGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCC  
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGCGCAGAGCTGGCACCCCTACT  
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG  
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCC  
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC  
 CGCCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
 AACCTGCCCCGAACCAAGGTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT  
 GCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGAGTCGCTCCATGGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC  
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG  
 GCAGCACAACGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGGCCCTTGCCCTG  
 CATCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGT  
 ACCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGGACAAA  
 GCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTT  
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTCGCCCTGGAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTTCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC  
 GAAGGTCACTGGAACGTCTTCTAGCCAGACCCCTGGAGCTGAAGGTCACGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAGACCTTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT  
 ATTATATATTAATAAATAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAAAAAAAA

1001-1002-1003-1004-1005-1006-1007-1008-1009-1010-1011-1012-1013-1014-1015-1016-1017-1018-1019-1020-1021-1022-1023-1024-1025-1026-1027-1028-1029-1030-1031-1032-1033-1034-1035-1036-1037-1038-1039-1040-1041-1042-1043-1044-1045-1046-1047-1048-1049-1050-1051-1052-1053-1054-1055-1056-1057-1058-1059-1060-1061-1062-1063-1064-1065-1066-1067-1068-1069-1070-1071-1072-1073-1074-1075-1076-1077-1078-1079-1080-1081-1082-1083-1084-1085-1086-1087-1088-1089-1090-1091-1092-1093-1094-1095-1096-1097-1098-1099-1100-1101-1102-1103-1104-1105-1106-1107-1108-1109-1110-1111-1112-1113-1114-1115-1116-1117-1118-1119-1120-1121-1122-1123-1124-1125-1126-1127-1128-1129-1130-1131-1132-1133-1134-1135-1136-1137-1138-1139-1140-1141-1142-1143-1144-1145-1146-1147-1148-1149-1150-1151-1152-1153-1154-1155-1156-1157-1158-1159-1160-1161-1162-1163-1164-1165-1166-1167-1168-1169-1170-1171-1172-1173-1174-1175-1176-1177-1178-1179-1180-1181-1182-1183-1184-1185-1186-1187-1188-1189-1190-1191-1192-1193-1194-1195-1196-1197-1198-1199-1200-1201-1202-1203-1204-1205-1206-1207-1208-1209-1210-1211-1212-1213-1214-1215-1216-1217-1218-1219-1220-1221-1222-1223-1224-1225-1226-1227-1228-1229-1230-1231-1232-1233-1234-1235-1236-1237-1238-1239-1240-1241-1242-1243-1244-1245-1246-1247-1248-1249-1250-1251-1252-1253-1254-1255-1256-1257-1258-1259-1260-1261-1262-1263-1264-1265-1266-1267-1268-1269-1270-1271-1272-1273-1274-1275-1276-1277-1278-1279-1280-1281-1282-1283-1284-1285-1286-1287-1288-1289-1290-1291-1292-1293-1294-1295-1296-1297-1298-1299-1300-1301-1302-1303-1304-1305-1306-1307-1308-1309-1310-1311-1312-1313-1314-1315-1316-1317-1318-1319-1320-1321-1322-1323-1324-1325-1326-1327-1328-1329-1330-1331-1332-1333-1334-1335-1336-1337-1338-1339-1340-1341-1342-1343-1344-1345-1346-1347-1348-1349-1350-1351-1352-1353-1354-1355-1356-1357-1358-1359-1360-1361-1362-1363-1364-1365-1366-1367-1368-1369-1370-1371-1372-1373-1374-1375-1376-1377-1378-1379-1380-1381-1382-1383-1384-1385-1386-1387-1388-1389-1390-1391-1392-1393-1394-1395-1396-1397-1398-1399-1400-1401-1402-1403-1404-1405-1406-1407-1408-1409-1410-1411-1412-1413-1414-1415-1416-1417-1418-1419-1420-1421-1422-1423-1424-1425-1426-1427-1428-1429-1430-1431-1432-1433-1434-1435-1436-1437-1438-1439-1440-1441-1442-1443-1444-1445-1446-1447-1448-1449-1450-1451-1452-1453-1454-1455-1456-1457-1458-1459-1460-1461-1462-1463-1464-1465-1466-1467-1468-1469-1470-1471-1472-1473-1474-1475-1476-1477-1478-1479-1480-1481-1482-1483-1484-1485-1486-1487-1488-1489-1490-1491-1492-1493-1494-1495-1496-1497-1498-1499-1500-1501-1502-1503-1504-1505-1506-1507-1508-1509-1510-1511-1512-1513-1514-1515-1516-1517-1518-1519-1520-1521-1522-1523-1524-1525-1526-1527-1528-1529-1530-1531-1532-1533-1534-1535-1536-1537-1538-1539-1540-1541-1542-1543-1544-1545-1546-1547-1548-1549-1550-1551-1552-1553-1554-1555-1556-1557-1558-1559-1560-1561-1562-1563-1564-1565-1566-1567-1568-1569-1570-1571-1572-1573-1574-1575-1576-1577-1578-1579-1580-1581-1582-1583-1584-1585-1586-1587-1588-1589-1590-1591-1592-1593-1594-1595-1596-1597-1598-1599-1600-1601-1602-1603-1604-1605-1606-1607-1608-1609-1610-1611-1612-1613-1614-1615-1616-1617-1618-1619-1620-1621-1622-1623-1624-1625-1626-1627-1628-1629-1630-1631-1632-1633-1634-1635-1636-1637-1638-1639-1640-1641-1642-1643-1644-1645-1646-1647-1648-1649-1650-1651-1652-1653-1654-1655-1656-1657-1658-1659-1660-1661-1662-1663-1664-1665-1666-1667-1668-1669-1670-1671-1672-1673-1674-1675-1676-1677-1678-1679-1680-1681-1682-1683-1684-1685-1686-1687-1688-1689-1690-1691-1692-1693-1694-1695-1696-1697-1698-1699-1700-1701-1702-1703-1704-1705-1706-1707-1708-1709-1710-1711-1712-1713-1714-1715-1716-1717-1718-1719-1720-1721-1722-1723-1724-1725-1726-1727-1728-1729-1730-1731-1732-1733-1734-1735-1736-1737-1738-1739-1740-1741-1742-1743-1744-1745-1746-1747-1748-1749-1750-1751-1752-1753-1754-1755-1756-1757-1758-1759-1760-1761-1762-1763-1764-1765-1766-1767-1768-1769-1770-1771-1772-1773-1774-1775-1776-1777-1778-1779-1780-1781-1782-1783-1784-1785-1786-1787-1788-1789-1790-1791-1792-1793-1794-1795-1796-1797-1798-1799-1800-1801-1802-1803-1804-1805-1806-1807-1808-1809-1810-1811-1812-1813-1814-1815-1816-1817-1818-1819-1820-1821-1822-1823-1824-1825-1826-1827-1828-1829-1830-1831-1832-1833-1834-1835-1836-1837-1838-1839-1840-1841-1842-1843-1844-1845-1846-1847-1848-1849-1850-1851-1852-1853-1854-1855-1856-1857-1858-1859-1860-1861-1862-1863-1864-1865-1866-1867-1868-1869-1870-1871-1872-1873-1874-1875-1876-1877-1878-1879-1880-1881-1882-1883-1884-1885-1886-1887-1888-1889-1890-1891-1892-1893-1894-1895-1896-1897-1898-1899-1900-1901-1902-1903-1904-1905-1906-1907-1908-1909-1910-1911-1912-1913-1914-1915-1916-1917-1918-1919-1920-1921-1922-1923-1924-1925-1926-1927-1928-1929-1930-1931-1932-1933-1934-1935-1936-1937-1938-1939-1940-1941-1942-1943-1944-1945-1946-1947-1948-1949-1950-1951-1952-1953-1954-1955-1956-1957-1958-1959-1960-1961-1962-1963-1964-1965-1966-1967-1968-1969-1970-1971-1972-1973-1974-1975-1976-1977-1978-1979-1980-1981-1982-1983-1984-1985-1986-1987-1988-1989-1990-1991-1992-1993-1994-1995-1996-1997-1998-1999-2000-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**FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902  
><subunit 1 of 1, 451 aa, 1 stop  
><MW: 49675, pI: 7.15, NX(S/T): 1  
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPFVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRRGPGTPAPTGLSAPLSFIPRHF RPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGLPLCILCTCEDGRQDCQ RVTCPT EYPCRHPKVAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

**FIGURE 87**

[illegible]

**FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGEGGASGRSP

**Signal peptide:**

amino acids 1-18

1007306.123101



**FIGURE 89**

[illegible]

**FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905  
<subunit 1 of 1, 406 aa, 1 stop  
<MW: 46038, pI: 6.50, NX(S/T): 2  
MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALERLAQCQDQSSRHAAELRDFKNKM  
LPILLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVVPFPWVG TGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN  
RTVVDSSVFAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLC LAKLDPQTLDT EQ  
QWDTPCPRENAEAAFVICGTLV VYNTRPASRARIQCSFDASGTLTPERAALPYFP RRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCACTCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
 CTCTCATGCTCAGTTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTTCTGTCTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTTACAGGGCCAGTTCTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAAATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT  
 GATAGAGACATCCAGTACTCTGTCACTCCTCGGCTGGTTCCCCCGGCCACAGCGAAGTG  
 GAAAGGTCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGTACAGATAGGAGATACCTTTTTTCGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
 GCATTGTTGGACTGAAGATTTTCTCTCCAAATTCAGTGAAAAATCCAGGCGAACTGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAACTGTAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG  
 GCGCTGGGAGTGTGCCGGATGATGTGGACAGGAGAAGGAGTACGTGACTTTGTCTCCCG  
 ATCATGGGTACTGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
 TTTATCAGCGTCTTCCCAGGACCCACCTACAAAAATAGGGGTCTTCTTGAGCTATGAGTG  
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTATACCTGACATGTCGGT  
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAATCCC  
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAGAGGCCCTCTTGGCAAAGGGCCTCTGC  
 AATCCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
 GTGAAATG**TAGGAT**GAAATCACATCCCACATTCTTCTTAGGGATATTAAGGTCTCTCTCCA  
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC  
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
 TCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
 AAAAAA

**FIGURE 92**

MALMLS LVL SLLKLGSGQWQVFGPDKPVQALVGEDAAAFSCFLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCR ISSQSYQK  
AIWELQV SALGSVPLISITGYVDRDIQLLCQSSGWFFRPRTAKWKGPQGQDLSTD SRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAELDWR RKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFRTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRRDDVDRRKEYVTLS  
PDHGYWVLR LNGEHLYFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATTPFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

**FIGURE 93**

GCGATGGTGC GCCCGGTGGCGGTGGCGGGCGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA  
 ACGAGGAGAGATGACTGACCAACC GACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
**CATGAGGAGCCTGCCGAGCCTGGCGGCCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG**  
 CCGTCGCCTCAGCCGCCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCGAGGTG  
 GACGCGTCGCGGGGCCCCGGGTTGCGGGGCGAGCCGAGCCACCCCTTCCTTAGGGCGACGGC  
 TCCCACGGCCCCAGGCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC  
 ACCACCTTTCAGGCGCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACCTC  
 GACCACCTCTCAGGCGCCGACCA GACCCGCGCCGACCACCCCTTTCGACGACCACTGGCCCGG  
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCGGACCCCGACCCCC  
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCACCCACCTGCGCACCGAGGCCCTC  
 TTCGCTCTCTCAGAGTATGTATGTAAC TGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCACAGGGCAGTGTGAGTGTCGGCCAGGTTATCAGGGGCTTCACGTGTAAACC  
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAAGTGAAGTTTATT  
 TTATTTTAGCAAGGGA AAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
 GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACCTTTTATCTCTTACTTTTATATGT  
 TATATTTAATGTG CAGGATTTAAAAACATCTAATTTACTGATTAGTCTCTCAAAGCAGTAG  
 AGTCGCCAATTTTCTCTGGGATAATTTCTGTAAATTT CATGGGAAAAAATTTATGGAAGT  
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA  
 ATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACTGGGGTACCCCTAATTTA  
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGTAGACCAAAAG  
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA  
 ATAATGTACTGTTATCTAAGCATTGCGTTGTACTGCACTGAAAGTAATTTATCTTTGACCT  
 TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT  
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACTGGGTATAACCCAAGATCTGCTGC  
 CACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTCCTCTCAAG  
 GTTGTGTGAAGATTAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGTTTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA  
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA  
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAAGTAGAAG  
 AGGCTGGGCGCGTGGCTCAGCCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGAAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGTCTCTACTAAA  
 AATACAAACAAATTAGCTGGCGGTGGTGCCACACACCTGTAGTCCAGCTACTCGGAGGCT  
 GAGGAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT  
 GCACCTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRSLSLGLGLALLCCAAAAA AVASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPITPPAAERTS  
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTPDLPSSSSSSVLPTPPATEAPS  
SPPPEYVCNCSSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

100730612301  
100730612301

### FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**CATG**GGCGGCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCAGGCCGTGTGTTGGGAAGACTGGACCTTGAGCAGCTTCTTTGGG  
CCCTGGTACGTGCTTGCAGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCTGTGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGAGCGCTGTCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGCGAAAACCTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC  
CTGGGCTTCTGTACAGT**TAGC**AGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGTGCTGCTCCCACTAGGGATGGCGCCACAGGGTCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTTC  
CAGACGA

**FIGURE 96**

MGGLLLAAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNRLRTLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

10017306.123101



**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
 GGCTGGATTTACCCTGGCCCAGTAGTTTCATGGCTACTGGTCCGGGAAGGGGCCAATACAGA  
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA  
 AGAAGTGATGCGGGGAGATACTTCTTTCTGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
 GCACCTTGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCTGTGAGCAG  
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
 CCGTCTCTCGGTGCTCACCTTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCGTGACCTGTGCCCC  
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
 ATTACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCCGGGGAGCTGGAGCCACAGCCCTG  
 GTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTACGCCT  
 CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT  
 TCTGCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
 ACAGATGAAGAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTTGTAAGATTACAGCCCTCAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
 CCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

**FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF  
REGANTDQDAPVATNNPARAVWEETDRFRHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
SIKWNKYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPPMISWIGTSVS  
PLDPSTTRSSVLTLPQPQDHGTS LTCQVTFPGASVTNKTVHLNVSYPPQNLMTVFQGDG  
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
CRKKSARPAAGVGDTGIEDANAVRGSSASQGPLEPWAEDSPPDQPPPPASARSSVGEGELQYA  
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATG**AAGACCCCTGTTCTCTG  
 GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCTTCACCCTGGAGGAGGAGGATATCACAGG  
 GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCAGGA  
 AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
 ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
 ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT  
 ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCCTGCTCCACATGGGAAAGCTTGTGGGT  
 AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
 ACTCTCGGAGGAGGACATTTTCAGCCCTGCAGACGGGAAGCTGCGTTCCTCGAACAC**TAGG**  
 CAGCCCCCGGGTCTGCACCTCCAGAGCCACCCCTACCACCAGACACAGAGCCCGGACCACCT  
 GGACCTACCCTCCAGCCATGACCCTTCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
 TTCCCCCAA

**FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTGLGAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL  
EATFTFMREDRCIQKKILMRKTEEPGKYSA YGGRKLYLQELPRRDHYIFYCKDQHHGGLLH  
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:****Signal peptide:**

amino acids 1-17

10017306-13-1001

STTCCGCAGATGCAGGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCAC  
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTGCAG  
TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACA  
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAGACACC CGCAATGA  
CATCATGCTGGTGAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACC  
TCTCTCAAGCTGTGTGCTACTGCTGGCAGCAGACTGCCATTCTCCGGTGGGGCAGCAGCTTC  
AGCCCCCAGTTACGCCTGCTCTCACACCTTGCATGCGCAACATCACCATCATTGACACCA  
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGGCCCTCTGGTCTGTAACAGTCTCTT  
CAAGGCATTATCTCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA  
CCCACCACAGCCCATCACCCTCCATTTCACCTTGGTGTTTGGTTCTCTGTTCACTCTGTTAAT  
AAGAAACCCTAAGCCAAGACCTCTACGAACATTCTTTGGGGCTCCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGGTTTCAAATCAGTGAGACCTGGATTCAAATTTCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAAACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA  
AAGACAGCTCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 102**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIW
AVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRCANITIIHQKCEAYPGNITDTM
VCASVQEGGKDCSQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

```

**Important features:****Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCTGCTGAGCCG**GATG**CCAAAAACCATGCATTTCCTATTAGATTTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGGAGAGACCAGAA  
GTGAAAATAGAAGTTTGCATCGTCCAGAAAAGCTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTGAAATTCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAATGTTTGTCTTGGTGTGGGCAAGTCATAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAAGCAAGATTCCACCGGATGCTACATTGATTTTTG  
AGATTGAACCTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTGTAGAAGATATTTTAAAG  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
GAACATA**TAGC**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AACCAAAAGTCATTTTCTCAAAGTTGATTTGCTATTTTTCCCTATGAGAAGATATTTTGA  
TCTCCCCAATACATTGATTTTGGTATAATAATGTGAGGCTGTTTGCAAACTTAAAAAAA  
AA

**FIGURE 104**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406  
<subunit 1 of 1, 222 aa, 1 stop  
<MW: 25794, pI: 6.24, NX(S/T): 1  
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG  
YLAKDGSKFYCSRTQNEGHGPKWFVLGVGVQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY  
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD  
KSYQDAVLEDFKKNDDHGDGFISPKYENVYQHDEL

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214



**FIGURE 105**

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACAAAACCTTCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAAACTATTCACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTCATTTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

**FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPFNASCVNNTHCTCNHGYTSGSGQKLFTFPL  
ETCNARHGGSRL

**Signal peptide:**

amino acids 1-18

1007706 1007706 1007706 1007706 1007706



**FIGURE 108**

MGLSIFLLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNFFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGFLVCGGVLQGLVSWGSVGPCGQDGI PGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

10017306.123109

CGGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
ACGAGACGACGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGACATGCTAGCCTGCCCTTGA  
GAGACCCGCTGGACTCCCCAGCCTTCCCCACCCCATACCTCCCTCCCGATCTTGTGTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTTGTGGTCAATTGAGGGTTTGTTTGTGTTT  
TCATCAATGTCTTTGTAAAGCACAATATTATCTGCCTTAAAGGGGCTCTGGGTTCGGGAATCC  
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
CTCACTTGGAGGAACAGCACTCTCCATCCTTTCAGAAAGTCCTCAAAGCCAAGTTCAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC  
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT  
CATCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCTTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGCAGCCCTACTGTCCCTTACTGGGCGAGCAGAGGGCTTCGGAGGCGAGAAGTAGGCGGAG  
GGGTTTGGGGGAAAGGTCACTCAGTCAGTCTGTTCCACCTTTTAGGAGGATACTGAGGGGAC  
CAGGATGGGGAATGAGGAGATAAATGCTCACGGCAAGTCAGCAGCACTGGTAAGCCAGA  
CTGAGAAATACAGGTTGCTTGCTCGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEinREFLCDQKYSDEENLPEKLTAFKEKYMFDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV  
MFEGKANESSPKPVGPPPERDIASLP

1017306.123101

**FIGURE 111A**

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCGCTCCTCCA  
 GGAGCGGGGCCCTGCACACATGCGCCCCGGGTGGGCAGGGGTGCGCGCCGCGTGCAGCGCC  
 CGCTTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTTGAAGTGGGCTTCCAGCCCTCGCTTGGCC  
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCTTCCGCGCGGTTTC  
 CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATATATACACAGGATC  
 ACCAAGATGGATCTTCTGTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAAGACAACCGATC  
 CAGCGTCATCGAGAGAGGCGCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCTGAAACA  
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
 GATTTGAGTGAACACAGATCCAGGGGATCCCGAGGAAGGCTTCCGCGGCATCACCGATGT  
 GAAGAACCTGCAACTGGACAACAACACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
 TGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTACCAGC  
 TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG  
 CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTACACTCT  
 GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCGAGAAGAAGGAGTACGTG  
 TGCCCGACCCCCCACTCGGAGCCCCCATCTGCAATGCCAACTCCATCTCTGCGCCTTCCGCC  
 CTCGACGTGACGAATAACATCTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTGCCCA  
 AACTTGGCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGGCATCCCTGCA  
 GGAGCCTTCAACCGAGTCAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCCGA  
 TATTTGCTCAGATGCTTCCAGGGCCTGAAATCACTCACTCATCTGTGCTATGGGAAACA  
 AGATCACCAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
 AATGCCAACAAAGATCAACTGCGCTGCGGGTGAAACAGTTTACAGGACTGCGAGAACCTCAACT  
 GCTCCTCCCTGTATGACAAAGCTGACAGACCTCAGCAAGGGGCTCTTCCGCCCTCTGCACT  
 CCATCCAGACACTCCACTTAGCCCCAAAACCATTTGTGTGCGACTGCCACTTGAATGGGTG  
 GCGGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGTGCGACAGCCCGCGCG  
 ACTCGCTCAACAACGCGCATCAGCCAGATCAAGAGCAAGAACTTCCGCTGCTCAGGCTCCGAGG  
 ATTACCGCAGCAGGTTGAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCGGAGAAGTGTGCG  
 TGTGAGGGCAGGATTGTGACTGCTCCAACAGAAAGCTGGTCCGCACTCCAAGCCACTCCC  
 TGAATATGTACCGGACCTGCGACTGAATGACAATGAGGTATCTGTCTTGAGGGCCACTGGCA  
 TCTTCAAGAAGTTGCCAACCTGCGGAAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
 CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCACT  
 GGAGACCGTGACCGGGCGCGTGTTCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA  
 GTAACCTGATCAGCTGTGTGAGTAATGACACTTTGCGGCGCTGAGTTGGTGAGACTGCTG  
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCAACACGCTTGCTCCTCT  
 GTCCACCAATAAACCCTCTGTCCAACCCCTTCAACTGCACTGCCACCTGGCCTGGGTGCGGA  
 AGTGGTTGAGGAAGAGCGGATCGTCAGTGGGAACCTCAGGTCGAGAAAGCAATTTTCTC  
 AAGGAGATTTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG  
 TAGCTGCCAGCTGAGCCGCGCTGCCCCGAGCAGTGACCTGTATGAGACAGTGTGGAT  
 GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGGCGATGCCCAAGGATGTGACCGAGCTGTAC  
 CTGGAAGGAACACCTTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
 TATTGACCTGAGGACAACAAGCATCAGCATGCTGACCAATGACACTTCAATACATGTCTC  
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGTCCAGCGCTTCAAC  
 GGGCTGCGGTCCCTGCGAGTGTCTAACCCCTCCATGGCAATGACATTTCCAGCGTTCTCGAAGC  
 CTCTTCAACGACCTCAGACTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG  
 ACTGCACTCTTGGTGGCTGTGCGAGTGGGTGAAGCGGGGTACAAGGACCTGGGATCGCC  
 CGCTGCACTAGCCCTGAGCCGATGGCTGACAGGCTCCTGCTCACCACCCCAACCCGCTT  
 CCAGTGAAGGGCGCTGGACATCAACATTTGGCCCAATGCAATGCTGCTCTCCAGCC  
 CGTGCAAGAATACGGGACATGCCACCAAGGACCTGTGGAGCTGTACCGCTGTGCTGCCCC

1007306 123101

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGTGTCTCCTGCCCTC  
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCAGATGACTGTGAGGACAACGACTGCCGAA  
 AACATGCCACCTGCGTGGACGGGATCAACAACACGTGTGTATCTGTCCGCTAACTACAC  
 AGGTGAGCTATGCGACGAGGTGATTGACCACCTGTGTGCCCTGAGCTGAACCTCTGTGAGCATG  
 AGGCCAAGTGCAATCCCCCTGGACAAAGGATTTCAGCTGCCAGTGTGTCCCTGGCTACAGCGGG  
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAGTGCCGCCACGCGGGCCAGTGTG  
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTG  
 AACACCCCCCAGGCTGCTTACTGACAGCCAGCCCATGCCAGCCAGTACGAGTGCCAGAAC  
 GGGGCCAGTGCATCGTGGTGACGAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG  
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAGACTCCTACGTGGAACCTGG  
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC  
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTTGGCACTGGAGCTGTACCAGGGCCACGT  
 GCGGCTGGTCTATGACAGCCTGAGTTCCTTCCAACCACAGTGTACAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTTTCAGAGTGTGGAGCTGGTGACGCTAAACAGACCCCTGAACCTAGTAGTG  
 GACAAAGGAATCCAAAGACCTGGGGAAGCTCCAGAAGCAGCCAGAGTGGGCATCAACAG  
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCCTCTCCGCTTGGCCAGGGCACGG  
 ACCGGCCTTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGACAG  
 GACTTCAAGGCCCTCCACACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTTGACCCGT  
 GTGCAAGCAGCGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
 GCTGGACCGGCCACTCTGCGACAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
 GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACCATG  
 GTGGGCCCAAGTGTGCCAGCCCAACCGCAGCAAGCGGGCGGAAATACGCTTCCAGTGCACG  
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGGGTGCCTCGCGTGTTT  
CTAAGCCCCCTGCCCGCCTGCCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
 ATGTGGGACCCCTGGTGATTACGATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA  
 AGAGAAATATTAAGTATATTGTAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAA  
 AAAAAA



**FIGURE 112**

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL  
 PELLFQSTPKLTRLDLSENQIQGIPRKA FRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL  
 TLNNNNISRI LVSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLQRRTVQGQTL CMAPVHL  
 RGFNVADVQKKEYVC PAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
 EIRLEQNSIKAIPAGAFQYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLVYGNKITEIAK  
 GLFDGLVSLQLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL  
 AQNPFFVCDCHLKWLDYLDQNPDIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS  
 SECMDLVQCEKCRCEGTIVDCSNQKLVRI PSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN  
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
 SNTDFAGLSSVRLLSLYDNRITTTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLRRR  
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRL  
 ALPRGMPKDVTLEYLEGNHLTAVPRELSALRHLLTIDLNNISIMLTNYTFSNMHLSTLIL  
 SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL  
 SEWVKAGYKEPGIARCSSPEPMADRLLLTPTTHRFQCKGPDINIVAKNACLSSPCKNNGT  
 CTQDPVELYRCACPYSYKGDCTVPINTCIONPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR  
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLQHEAKCIPL  
 DKGFSCECVPGYSGKL CETDNDDCAHKKR HGAQCVD TINGYTCTCPQFGSGPFCEHPPPMV  
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHS  
 VELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
 HGCIEHRINNELQDFKALPPQSLGVS PGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEYGGDLCDNKNDSANACSAFKCHHGQCHISD  
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVI RQKGYASCATASKVPIMECRGGCGPQCCQ  
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA  
GACTCAACTGAGAACTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTTCTCGAGGGCTGGCCTG  
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGACAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATGTTAAAGA  
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGA AAAAAGGCTGTGAGGTTTCCTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCTATCTTGTCCCGTTTCCTCCCAATA  
TTCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
TTAAATGTC

1007706 23404



**FIGURE 115**

CAGGCCATTGTCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAAACTTGTACATGGCTCCC  
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
 ACATTCAAGTCCCTGTCTCACATAGACCCCTGATGTCCTCTATCCATCTCTAAATGTACCAG  
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAAGATTGACATCCCAAGATTGGGAGAGGGTTTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCTGGGAAATGTGGAACATTATCAGGAATTGAAGAAAAATGGTCCAAC  
 AGTCCGACCTTGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAAATCTCC  
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCATTGTGGCATTGTCCC  
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT  
 CCATTGACCACAGTGTCTACAGGGTTCTGTGTGAGCCTGACCCGGTGCCTTCTCAGAAGCA  
 ATAGAAAAGTTTCATCCGTGAACCTTCCTTAAAGCCACCATTGGGCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAAATTTTCCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC  
 TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC  
 CAGTTTTGAAAACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA  
 CTTGAGTCTTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
 TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTAAGTGTGTATCATTATCAA  
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAAT  
 CCACCGAAGTGTTCACTGTCTCTGTTAGGGAATTTTGTGTCCTGTCTTTGCCTGGATC  
 CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAAATTTGTATTTTGCACACTGAGATATAA  
 TAAAAGGTGTTTATCATAAAAA

**FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRRLARRRKILFYCHFPDLLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGR LTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

1007306-12101

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATGT**TTGGACTTCGCGATCTT  
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
 AAGCTGCAGGAATTCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
 GTGAATAGTGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCCTGTGGT  
 CTCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAACCATGCTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT  
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
 CTTCAGAGAAGATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTCAC  
 TTGATAAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC  
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA  
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTGATGATGTGCTTTGTGAAACTGTTGCAACTGCCA  
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT  
 CCTAGAGAGACCTCGTCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCTCT  
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
 GTACTTCTTAGTGATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
 AT**TAAA**ATTTTATACATTTAAATCATTTGTTAAATTGATTGAGGAAAAACACCATTTAAAAA  
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAACACCTATTGTAC  
 TTAA

**FIGURE 118**

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVSLGTVDLVKQHINPNKTSDPFETMLKSLRLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLLKSEELLKWLSTYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWSEIGKGFLDGS�DKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVCETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLLVLYALGVVL  
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCGGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCTCCGAGGGGCCATGGGCCGGGTCTCAGGGCTTGTCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGACAGCAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTACAGCTGG  
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT  
TCTGCAGTGCCCTTCAGCTGTCACTGAAATGGCTTTATTTCGTACCGTCTTTGGGCTGAAA  
AAGAAACCTTCTTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCTTGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA  
ATTAAAAAAAAAAAA



**FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT  
EMALEVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

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**FIGURE 121**

TCCCGGACCCCTGCCGCCTGCCACT**TATG**TCCCGCCGCTCTATGCTGCTTGCCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGGCTCGTGCCAGC  
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGTAC  
AACTTCTTGATTGGAGAAGACGGGCTCGTATACAGGGCCGTGGCTGGAACCTTACGGGTGC  
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTATGGGCAACTACATGG  
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCAATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCACTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCC**TGAG**GGCC  
CTGCTGATCCGCACTCCATCTCCCTCCCATGGCCAAAACCCCACTGTCTCCTTCTCCA  
ATAAGATGTAGCTC

**FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

1001/205 12310

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGTGCTGCTTCTGTTCTTCTGCTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCTCTCCCGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCATGGCCAATTCACACTCT  
 CCTAGGGTGCTGGCCCCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATTGGCAA  
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAAG  
 GCCTCCAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCGGACCTC  
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC  
 TGGG**TGA**CCCCGGGCGAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGGAGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC  
 ACAGCCCATCCGCGTGCTGTGTGCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCC  
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGCCGAGAG  
 GCATGTGCTGGATCTGTTCTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTT  
 GCCCCGGGGCA

10017306-123101

**FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521  
><subunit 1 of 1, 252 aa, 1 stop  
><MW: 28127, pI: 8.91, NX(S/T): 5  
MQLTRCCFVFLVQGSLYLVICGDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR  
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY  
YPSG

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA  
GGCAGGGCTGATTCTTTGGGCGGAGGAGTAGGGTAAAGGGTCTGCATGAGTCCCTTAAAG  
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
TGGTGGAAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCGAGCGTGTGCACTAGCCGCTAG  
CATCTTCCCAGACCCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
GGCTGCGGCTGCCACACGGCTCACC**ATG**GGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
GCCGTGCTGCTGGTCCCTACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
GCTCCTCTTCCCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG  
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
CGATCAGATCCTGGTGAATGTGGGTAATTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA  
GAAAAGGAATTTACAGTTTCAGTTTTACGTGATTAAGTCTACAGAGCCAACTATCCAG  
GTTAACTTTGATGTTAAATGGAAAACAGTAATATCTGCCCTTTCGCGGGGACAAAGATGTTAC  
TCGTGAAGCTGCCACGAATGGTGTCTGTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
AACTGGAGAAAGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG  
TTCCCCCTAT**AGG**GATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
ACAGTCAAAGCTGTCTGCAAGACTTATTTCTGAATTTTATTTCTGGGATTACTGAATTAGT  
TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
AAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTGTTCTTGTA  
AAAACCTGGATTTTTTTTTTTCAGTAACGGTATTATGTTTTCTCTTAAATAAGGTAATGAA  
TGGCTTGGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAA  
GAATGCTTCATAGTTGATTTTTAATTGTATATGTGAAGAGTCATATTTTCCAAGTTATATT  
TTCTAAGAAGAAGATAGATCATAATCTGACAGGAAAAAGTTGCTTACCCAAAATCTAAG  
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACTTTATTGC  
TCAACTTTAATTAATAAGATTGATAATAACCACTTTATTAATAAACCTAAGGTTTTTTTTTT  
TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACCTCTTTAATTGTA  
TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAATTTAGTGAATAT  
CTTGCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAGA  
TTAATATATGTTAAAAA

10017306-126109

**FIGURE 126**

MGSGRRALSAPPAVLLVLTLPGLPVWAQNDEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI  
SVRAANSKVAFAVAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVVFAPRKGIIYSFSF  
HVIKVIYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

100730-127-127

**FIGURE 127**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
 GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC  
 TTTCTTCTGGTTGGTGTCTCTACTGATTTCTGTCCTTGTTTGGTTCATGGCAAGAGTCATTA  
 TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
 TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
 GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
 TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTGGGG  
 CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC  
 GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA  
 AAAAGTGGGGCATCCTCCTTATCGTTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
 ATAAGTTCATTATATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGTCTGAGGCAC  
 CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
 ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA  
 ACCGCAGACTACATCTTTAGAGGAAGCACAACCTGTGCCTTTTTCTGAAAATCCCTTTTTCTG  
 GTGGAATTGAGAAAGAAATAAACTATGCAGATA



**FIGURE 128**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFTAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNLTSLGPGTVGIHGDS PQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLLCQDKN
FLLYNQSR
```

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 129**

CGGCAACACGCGCCGCCACACCGCTGCCACTGCCGCCCTGCCGGGGC**ATG**TTGCGCTCTGGGCTTGCCCTCT  
 TGGTGCTCTTGGTGGGCTCGGTGAGAGCCATCTGGGGGTTCTGGGGCCCAAGACCTCTCGCAAGACGCGG  
 AGTTTGAGCGCACTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTCTCAACCATCTGCTGACCC  
 GCAACGAGCAGAGGGGCGTGGTGTGTCTGTGAACGTCCTGAACAGCAGAGGGGGGCGCCGTGCTGTCTGTGG  
 TCGCCGAGAGGAGGCTGTGGTGTCTCTCCAGGTGCCCTAATCTCTGCGAGGGATGTTTTCAGCGCAGTACTCT  
 ACCAAAAAGTGGAACGAACCTGTGTGAGCCCCCACCAGAATGAGTCGGAGATTCAGTTCTTCTACGTGGATG  
 TGTCCACCTGTCAACAGTCAACACACATACAGCTCGGGTCAGCCGATGGACGATTTTGTGCTCAGGACTG  
 GGGAGCAGTTCACTCTAATACCACAGCAGCAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGCGCTGGACT  
 CGGTAAITGTCAAGGTGACTCTCAACAAAGGCCCTTCCCTGCTCAGTCACTCTCCATTCAAGATGTGCTGTGCTCTG  
 TCTATGACTGGACAACACGTAGCCCTCATCGGCTGTACAGACGATGACCAAGAGCGGCCATCACCGTAC  
 AGCGCAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT  
 CCGTGCCCTTCTACCCCTTCGCAAGATGAACCGGTGATCAAGGGCACCGCAGAAAAACCTGTCACTGCTGG  
 TGCTCAAGCAGTCAGTCTGAGGCATACGTCACTGGGATGCTCTTTTGCTGGGTATATTCTCTCCTTTTACC  
 TGCTGACCGTCTCTGGCCTGCTGGGAGAACTGGAGGCAGAGAGAAAGACCTGCTGGTGCCATTGACCGAG  
 CCTGCCCAAGAAAGCGGTCACTCGAGTCTGGCTGATTCTTTCTGGCAGTCCCTTATGAGGGTTACAACCT  
 ATGGCTCCTTTGAGAATGTTTCTGGATACCGATGGTCTGGTGACAGCGCTGGCATTGGGACCTCTCTTAGC  
 GTTACAGGCGCCGCTCTTTGAACCTGTAGGTACTCGGCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG  
 ACTACGACATCTGACCGACATCGATTCCGACAAGAAATGTATTGGCACAAGCAATACCTCTATGTGGTGACC  
 TACGCAAGAGCAAGCAGGCTGTCTGGGAAAAAGTACCAAGTCTACTTCTACGCCATGGCCACCATTTGCTGTCT  
 TCTATGCCCTTCTGTGGTGACGTGTGTGATCACTACAGACGGTGGTGAATGTACAGGAGAAATCAGGACATCT  
 GCTACTACACTTCTCTCGCCCAACCCACTGGGCAATCTCAGCGCACTTCAACCAACATCTTCAAGCACTGGGGT  
 ACTACTCTGCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCAACACCGGGCCCTGCTCGGCA  
 ATGACCTCTGTGGCTGGAAATGTGGATCCCCAACACTTTGGCTTTTCTACGCCATGGCCACCGCTGATGA  
 TGGAGGGGCTGCTCAGTGTCTGCTATCATCTGTGCGCCAACTATACCAATTTCCAGTTTGACACATCGTTTATG  
 ACATGATCTCGCGGACTCTGCATGCTGAAGCTCTACAGAAAGGGCACCCGGACATCAAGCGCCGCTCAGATG  
 CCTACGCTGCTGGCCATTTGGCTCTCTTTCTGTGCTGGGCTGCTTTTGGCAAGGACACAGCGGCTTCT  
 GGATGCTCTTCTCATCATTCACATCATCGCACCTGCTCTTCAAGCAGCAGCTATTACATGGGCGGCTGGA  
 AACTGGACTCGGGGATCTTCGCGCGATCCTCCAGTGTCTTACACAGACTGCATCCGCGATCGACGGGCGCTCG  
 TCTACGTGGACCGCATGGTGTGCTGGTGTGATGGGCAACGTCACTAATGCTGCTGGCTGCTATGGGCTTAGCA  
 TGGCGCCCAATGATTTGCTTCTACTTTGTTGGCCATTGGCATCTGCAACCTGCTCTTACTTGCCTTTTACA  
 TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGATCGTTTGACCTCCGCTGCT  
 GGGGCTTCGGCTCTTCTTCTTCTCCAGGACTCAGCACTGGCAGAAAAACCCGTCAGATCGAGGAGACACA  
 ACCGGGACTGCATCTCTCGACTTCTTGACGACCAGACATCTGGCACTTCTCTCTCCATCGCCATGTTG  
 GGTCTTCTGCTGCTGCTGACATGGATGACGACCTGGATCTGCGAGCGGGAAGATCTATGTTCT**TAGC**  
 AGGAGCTGGGCCCTTGCCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTATAGACCGGTCATCTGTCTGTGT  
 GTGGGATGAGTCCCAACCGCTGCCAGCATGGATGGCAGGACAGCAAGCTCTAGCTTAGGCTTGGCT  
 GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCGAGGACAGGCTGCTCCCTGGAACCCCT  
 AGATGTTGGCCAATTTGCTGCTTTCTTCTCAGTGTGGGCCCTCCATGGGCCCTGTCTTTGGCTTCCATT  
 TGCTCTTCTCAAGAGGAAGATGAAGAGGACACCTCCCATTTTATGCTGCTATTTGGCCGTCTCTCTCCCC  
 ACAATGCCCACTGGAGCTGGAGCTTGAAGCCTCTTTTCTCCCACTCTCCCATCGAGGGCTAGTCTGGGGCTGA  
 ATCTCTGCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCTAGCTGCCATTCCAGTCAAGC  
 AGGATGAGGCGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTTGTGCTGAAGCCTCGAAGGGG  
 CCTGGGACGTGCGTATTTCTTCTCCTGACCTGTGTCAAGGCTGGCTCTTTAGCAATCGCTCAGGCCAAT  
 TTGAGAACCGCTTGTATTCAAGAGGCTGAATTCAGAGCTCACTCTCATCCCATCGCTCCAGACTGATGCG  
 AGCAACAGGACTGAGGGGGAAGCGCTCACCCCTTCCTTCTCTTTCCAGGCCCTTAGTCTTGCCAAACCC  
 AGCTGTGGCCCTTTCAGTGCCATTGACACTGCCCAAGAATGTCCAGGGCAAGAGGAGATGATACAGAGTTGAG  
 CCGGCTTCTGCTCCACAGCTGTGGGCACCCAGTGCTCACTTAGAAAGGGGCTTCAGGAAGGATGTGCTGTTT  
 CCGCTCACTGTGCCAGTCTAGTCACTGCTCTAGGACACAGGCTGGCTTCTAAGTTTCCGTCCAGTTCCAGGCA  
 AGTTCTGTGTAGTACTGACACATACCTATGAACCTTGGAGTTTACAAAGAAATGCCCGAGCTCTGGGCAC  
 CTGGCCACCTGTGCTCTGGATCCCTCTGCTCCACCTGGTCCACCCAGATGCTGAGGATGGGGAGCTCAGG  
 CGGGGCTCTGCTTTGGGATGGGATGTGTTTTCTCCCAAACTGTTTTATAGCTCTGCTTGAGGGCTGG  
 AGATGAGGCTGGTCTGATCTTTTCTCAGAGCTCTCCATGCTATGTTGCAATTTCCGTTTCTATGAATGAAT  
 TGCATTCATAAACAACAGCACTCAAAAAAAAAAAAAA

**FIGURE 130**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLDDNNVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLLPFYPFAEDEPVDQGHQRKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVLAIDRACPESGHPRLVADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIIATIAVFYALPVVQLVITYQTVNVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHGFLFYAMGTALM
MEGLLSACYHVCPNYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKNTAFWIVFSIIHIIATLLSTQLYYMGRWKLDSGIFRRILHVLVYTDICIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALEFFQGLSTWQKTPAESREHNRCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDDLTQVRDKIYVF
```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGCCCTGCGCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTTGGGCGCTGGAGGGCCTGTCTCTG  
 ACC**ATGGT**CCCCTGCCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTCCAGAAAATATGGTGGAAATTTCCCTTTATACC  
 TGACCAAGTTGCCGCTGCCCGCTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCA  
 GGCAGGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACACG  
 GGCCTTGACCAGAGAGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG  
 GACATGTCTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGGAATGACCAAGGTG  
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCGGGGTACAGGCCTGGCATCCC  
 CTTCTCTTCTTGGAGGCTTACAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
 TCCACATCTGAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGCTGTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGGCACTG  
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCCATACCCGCCACCATGGCCCCAGGTACACTGGAGTGGGGTGATGT  
 GCATATCACTCAGTGAGAGCCATCCCCCGGACCCCTTTGAAGTGAATGCAGAGGGAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
 TGACAACGTGCGCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCAC  
 CAGGTACTGAAGTGACTAGACTGTGACGAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC  
 CACGTTGTGATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
 GGTGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCATCCGAGCAGGCCAGAAC  
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCCGACAGGGGTGGCTTCAGCAGCACGTGT  
 GAAGTCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTTTCACTCATCTCCAGAT  
 TGGGCCCTAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCCCTTCCGCCCTCATGGATTTTGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACACCCCCAAGTTGGACAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCC  
 AGCCGGCTCTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT  
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCCGGGGAGGTGCACACC  
 GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCACGGA  
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAAGACCATG  
 GCTTGAGCTGAGTGGACCCAGCAGAGGACCCGATCGGCCAGTGGGCACGGTCCCTACAGC  
 TTCACCTTGGTCCCAACCCACGGTGCAACGGGATTTGGCGCCTCCAGACTCTCAATGGTTG  
 CCATGCCTACCTCACCCTGGCCCTGCATTTGGTGGAGCCAGTGAACACATAATCCCGTTC  
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTGCAAC  
 GTGGAGGGGACGTGATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTCCGG  
 AGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCTCTATTTCCACCC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCTGCCCCCTGAAGGGG  
 ACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGCCCAAGCACAAGATCCAGAGGGGACAGGACAGATAGAAGAGCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATACCATACACAGGCATGTCTGACAGCCTGGACCAAC  
 TTTATGGACTGCCCATGGAGTGCTCCAAATGTCAAGGTGTTTGGCCAAATAAAGGCCCA  
 GAGACTGGCTGGGCCCTTGGGAAAAA

**FIGURE 132**

MVPAWLWLLCVSVQALPKAQPaelSVeVPENYGGNfPLYlTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGfLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPfLFLEASDRDEPGTANSDLRFHILSQAPAQPSpDMfQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSIIESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLMdENDNVpICPPRDPTVSIPELSPPGTEVTRLsAEDADAPGSPNSH  
VVYQLLSPePEDGVEGRAfQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGfSSTCE  
VEVAVTDINDHAPEfITSQIGPISLPEDVEPGTLVAMLTADLEPAfRLMDfAIERGdTE  
GTfGLDWEpDSGHVRLRLCKNLSYEAAPsHEVVVVVQsVAKLVGPgPGPGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSfLLTIQPSDPISRTLRFSLVNDSEGWLCIEKfSGEVHTA  
QSLQGAQPGDtyTVLVEAQDTALTlAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTlALHWVEPREHIIPVVVSHNAQMWQLLVrVIVCRcNV  
EGQCMRKVGRMKGMPTKLsAVGILVGTlVAIGIFlILiIfTHWTMSRKKDPDQpADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTGGAAGCTCAATTTCTGGAAATCTCCCTCTCCT  
 TCAATCGGCCTGTGGATGTCTTGGTCCCATCTGTCACTCTGCAGGCATTAAATCCTTCCTG  
 AGATCCCAGGGCTTAGAGTACGAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAAATGA  
 AGATGATGAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAAATTGCCGCAGACTTTCTCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTCTGTTGAAAACCGGCCGATGTATGTAAGATT  
 CAGCACTGGGAAAGCGGTGAGGCGCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCGAG  
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGTGCTGTGGCCAATCC  
 TGATGGATATGTGTATACTCAAACCTAAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTGTCTGACCCAAATAGAACTGGAACGCTAGTTTTGACAGGAAG  
 GGAGCCAGCGACAACCTTGTCTCCGAAGTGACCATGGACCCACGCCAATTCCGGAAGTGGA  
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCAAGTGC  
 GAGGAATCGACAGGTGGCGAGGGCTTGCGGCCAAAAGCTCTGGCTTCTGTGTGGGCCACTGA  
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGGAGCATCTGACTGGG  
 CGTATGACAAAGCGTCAAAATTTGCATTACATTTAGTTGAGATACCGGAGATCCCGGACCTATGGC  
 TTCCTCCTGCCAGCTAACCAGATCATCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGGCAACCTCTACTAGCGCATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTTTCTTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTGTCTTGGCGGTGTCCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTTTGGTCTGT  
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGTCTGGCTGGGCGGCTGCACCTC  
 AGCATCACCCCTTCTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC  
 TGAGATGATTCTCTACCCCTCATCCACATCTAGCCAAGCCAGTGACCTTGTCTTGGTGGCACT  
 GTGGGAGACACCCTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTCTTTAATTTT  
 TCGCAGTCTTCTTGGAAAATATTTTCTTTGAGCAGCAAACTCTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTGTCTTTGTGTGCC  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTACCCACAACCTCTGCCCTTGGGTTCGAAGCA  
 ATTCTCCTGCCCTCAGCCTCTTGTAGTAGCTTGGTTTATAGGCGCATGCCACCATCCTGGCTA  
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA  
 ACCCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCGGCTCCCTCTTTTATAGGCTGAATACAAAGTAGAAGATCACTTTCTCTTAC  
 TGTGCTGAGAATTTCTAGATACTACAGTCTTACTCTCTCTTCCCTTTGTATTACAGTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTCAGGATGGTGAAATATCCCATCTGCTCTAATGGGCTTACCTCCT  
 CTTTGGCTTTTGAACCTACTTCAAAGATCTAGGCCTCATCTTACAGGTCTCAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCATTCCCATTTGTGCTGTGGTGTATCTCTGTT  
 TCCTTGTCTTGGTTTTGT  
 GCTCTCTATTTTGTATCTTGACCACAAGTTCTTAAGTAGAGCAAGAATTCATCAACCAGCT  
 TGCTCTGTTTTTCACTTCCCTCAGCACGTACCATCTGTCTTTTGTGTGTGTGTGTGTGTGT  
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAATCTTAACTCCTGCCCTAGGATTTGTACA  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

**FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFRLSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPPAVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDFTIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLV

**Signal peptide:**

amino acids 1-16

**FIGURE 135**

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCAAA**ATG**  
 GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC  
 CCCGGCCAATGCCCCAGTGCATACCCCGCCCTTCTCCACAAAGAGCACCCCTGCCTCAC  
 AGGTGTATTCCCTCAACACGACTTTGCCTTCCGCCATATACCGCAGGCTGGTTTTGGAGACC  
 CCGAGTCAGAACATCTTCTTCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT  
 TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCAGGGCCTGGGCTTCAACCTCACACACA  
 CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCACAGC  
 AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC  
 AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTCTACAGATTTCTCCA  
 ACCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCAAGGGAAGGTT  
 GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTT  
 TAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATATACAAGAAAGAATCTCCCATCTCTGG  
 TGGGCGAGCAGGTCACGTGCAAGTCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGG  
 GTGGATACAGAGCTGAATGCTTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT  
 CTTTGTCTCCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACAC  
 TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTATCCCCAGATTTTCC  
 ATTTCTGCCTCTTACAATCTGGAAACCATCTCCCGAAGATGGGCATCCAAAATGCCTTTGA  
 CAAAAATGCTGATTTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCC  
 ACAAGGCTGTGCTGGATGTCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAG  
 TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCTT  
 GATGATGATTACAAATAAAGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAATCCCA  
 CTAATCTC**TAG**GTGGGAAATGGCCTGTTAACTGATGGCACATTTGCTAATGCACAAGAAATAA  
 CAAACCACATCCCTCTTTCTGTTCTGAGGTGCATTTGACCCAGTGGAGCTGGATTTCGCTG  
 GCAGGGATGCCACTTCCAAGGCTCAATCACCAAAACCATCAACAGGGACCCAGTCACAAGCC  
 AACCCCATTAACCCAGTCAGTGCCCTTTTCCACAAATTCTCCAGGTAACTAGCTTCATG  
 GGATGTTGCTGGGTTACCATATTTCCATTCTTGGGGCTCCAGGAATGGAATAACGCCAAC  
 CCAGGTTAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAACTAAAATATGAAT  
 TCAA  
 AAAAAA



**FIGURE 136**

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSAFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPISIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVSENRFTLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

10047306.12101  
1012179927101

**FIGURE 137**

GGCTGACCGTGCTACATTGCGCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGTGTCCACAGC  
 CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGAGCCACGCTCCTGGAAGACCAG  
 CCTTTATCTCTTACCCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAG  
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCAGGCCACAAAGAGACAG**TGA**AGATGC  
 AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTC  
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC  
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCA  
 GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTTCATACAACTCCAGTGGG  
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA  
 CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC  
 CCTCCAGTGGGGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC  
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA  
 GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCA  
 GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC  
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG  
 CACAACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAAGACCTCCAATGGGG  
 CTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCAGCACAGCCACCAAC  
 TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGC  
 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCTAGCA  
 CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCCAGCCACCAACTCTGAG  
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATCTGAGTCCAGCACACCCCTCCAG  
 TGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCA  
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG  
 ACAACTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGC  
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT  
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATCTGAGTCCAGCACAACT  
 TCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTCAGGCTCTGGAAC  
 AGCAGCTCTGACTGGAATGCACAACTTCCCATAGTGCATCTACTGCAGTGTGAGGCAA  
 AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATACCCCTGGTCTCGGTTGTGGCG  
 GCCGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCTGTCCCTGAGAAACAC  
 CTTTAACACAGCTGTCTACCACTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG  
 GGAATCATGGAGCCCCCAGGCCAGGTGGAGTCTTAACCTGGTTCTGAGGAGACCAAGTA  
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCT**TGAG**CAGCCCCGAAGCAAG  
 TGCCGCATTCTCAGGAAGGAAGAGACCTGGGCACCAAGACCTGGTTTCTTTTCATTTCATC  
 CCAGGAGACCCCTCCAGCTTTGTTGAGATCCTGAAAATCTTGAAGAAGGTATTCTCACC  
 TTTCTTGCCTTTACCAGACACTGGAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA  
 ATACATCTCATCTAACACACAGGACAAAGAGAAGCTGTGCTTGCCCGGGGTGGGTATCTAG  
 CTCTGAGATGAACCTCAGTTATAGGAGAAAACCTCCATGCTGGACTGCATCTGGCATTCAAAA  
 TCTCCACAGTAAATCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAA

**FIGURE 138**

MKMQKGNVLLMFGLLHLLEAATNSNETSTANTGSSVSISSGASTATNSGSSVTSSGVSTATI  
 SGSSVTSNGVSIIVTNEFHHTSSGISATNNEFSTASSGISIATNSESSTSSGASTATNSE  
 SSTPSSGASTVTNNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
 TTSSGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTT  
 SNGAGTATNSESSTSSGASTATNSDSTVSSGASTATNSESSTSSGASTATNSESSTSS  
 GASTATNSDSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTSSGA  
 NTATNSESSTVSSGASTATNSESSTSSGVSTATNSESSTSSGASTATNSDSTSSSEAT  
 ATNSESSTVSSGISVTNSESSTSSGANTATNSGGTATNSAGSGTAALTGMHTTSHSASTAV  
 SEAKPGGSLRPWEIFLITLVSVVAAGVLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHLGLP  
 GPGGNHGAPHRPWSPNWFWRPVSIIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGCC  
CTGCTTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCAGCG  
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACGGGC  
AAGGAGTTGGACAAAGCGCTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACACGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCCTTTCATCAACTTCCGCGCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTGCGCGTTGTCAACGACGTGAC  
ATGACCTGGAGGGGTTGGGGTGGGGGACAGGTTTCTGAAATCCCTGACAGGGGTTGTACTG  
GGATTGTGAATAAACTTGATACCA

**FIGURE 140**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHIGIQAGKEAEKLGHVNNAAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

[illegible]

**FIGURE 142**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min.ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF
EAEHISNITYALLLSRDGRTLIVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLDEGKGRCF
FDPNFKSTALVVDGELYTGTVSSSQGNDPAISRQSRLRPTKTESSLNLWQDPAFVASAYIPE
SLGSLQGDDDKLYFFFFSETGQEFEFFENTIVSRIRICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSPQDWRDRLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHFPVTPRPGACITNSARERKINSSQLPDRVLNLFKDHFLMDGQVR
SRMLLLQPPQARYQRVAVHRVPLGHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSSGSSCKHVSILYQP
QLATRPIWQIDIEGASAKDLCASSVVVSPSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATR
LWLNRNGAPVNASASCHVLP TGDLLVGTQDQLGEFCQWSLEEGFQQVLVASYCEPVEDGADVQ
TDEGGSVPVPIISTSRVSA PAGGKASWGDALSGYKEFLVMCTGLFVLAVLPLVFLFLYRHRNSM
KVFLKQGECA SVHPKTCFVVLPPETRPLNGLGKPPSTPLDHRGYLQSLSDSPPGARVFTSEKR
PLSIODSFVEVSPVPCPRPRVRILGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

**FIGURE 143A**

CTAAGCCGAGGATGTGCAGCTGCGGCGCGCGCGCGGCTACGAAGAGGACGGGACAGGCGCGGTGCGAAACCGA  
 GCCCAGCCGAGCGGAGGACCGCGGCGGAGCGGAGCCCGGACTCCTGCGCCGCGCGCTGCTGCGCGGTG  
 TGCCGCGCCCGCGTCCCGCGCGCGAGCGGGAGGAGCGCGCCGACCTCGCGCCCGAGCGCGCGCTAGCGCGCGCG  
 CGGGCATGGTCCCTCTTAAAGGCGCAGGCGCGCGCGCGCGGGGCGGGTGTGCGGAAACAAAGCGCCGCGCGGGG  
 CCTGCGGCGCGGCTCGGGGCGCGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCTGCCGGGCGCGGCTCG  
 CGCGCATAGGCGGGCTGGCTCCTCGTGGCGGGGGCAGCGGGCTGAGGCGCGCGCGGAGCTCGCGCGCGCGCG  
 GCGCGCGCGCGCGCGCGCGCGCGGAGCGCGCGCGGCTAGCGCGCGCGCGCGCGCGCGCTGGCTCAGCGTGC  
 TGTCTGGGCTCTGCTGGGCTCTGCTGCTGGCTCGCGGCTCTGCTGCCCGGGCTTCGAGATGAAAGCGAGCGG  
 GCCCAGCGCGCGCGCGCGCGCGGAGGCTGCGGCTCGCGCGAGCGCGCGCTCCGAGCGCGCGCGCGCGCG  
 CGGATGCGCGCGCGCGCGCGCTGCGCGCGCGCGCTCGGACCCAGATGGCGCGCGCGCGCGAGAGAACTTTCTCT  
 TCGTGGGATCATGACCCGCCAGAAATACTGCAGACTCGGCGCGTGGCGCGCTACGAGAACTGGTCCAAAGACA  
 TTCCTGGGAAGTTCACTTCTCTCAAGTGAGGTTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG  
 GTGTGGAGCACTCCTACCGCGCCGAGAAGAAGTCTCATGATGCTCAAGTACGATGACACCACTACTTGGACA  
 AGTATGAATGGTTATGAGAGCAGATGATGACGTGTACATCAAGAGAGACCGTCTGGAGAATCTCTGAGGAGTT  
 TGAACAGCAGCGAGCGCTCTTCTTGGGAGACAGGCTGGGCGCACCGAAGAATGGGAAAACCTGCCCTTG  
 AGCCTGTTGAGAATCTGCTATGGGGGGCTGGCGTGATCATGAGCGGGAGTGCTTCGGAGAATGGTCCGCG  
 ACATTGGCAAGTGTCTCCGGAGATGTACACCACCATGAGGACGTGGAGGTGGGAAGGTGTCTCCGAGGTTT  
 CAGGGGTCAGTGTCTGCTGCTGTATGAGATGCGGCGAGCTTTTATGAGAAATACGAGCAGACAAAGAGGGT  
 ACATTAGAGATCTCCTAATACGATTAATTCACAAAGCTATACATTACACCCCAACAAACCCACCTACCAT  
 ACAGGCTCCACAGCTACATGCTGAGCGCGAAGATCTCCGAGCTCGCGCATCGCAATACAGCTGACCCGGGAA  
 TTGTCTCTCAGCAAAATACGACACACAGAAATTCATAAGAGGAGCACTCCAGCTGGGAATCCCTCCCTCTTCA  
 TGGAGTTTACGCCCCGACGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAATACTTGTATTCCGAG  
 TTGACGGGACGCCCTCTCGAAGAGCAATGGACTCCGCCAGAGGAGGACCTTGGACAGTTGTCTGACGAGGTCA  
 TGGAGATCATCAATGGCCACCGAAGACAGAGGCGCATCATGACTCAAAGAGATCCAGTACGGCTACCGCC  
 GGGTGAAACCCCATGTATGGGCTGAGTACATCCTGGACCTGCTGCTCTGACAAAGAGACCAAGAGGGAAGAA  
 TGACGGTCCCTGTGAGGAGGACGCGTATTTACAGCAGACTTTACAGCAAAATCAGTTTGTGGAGCATGAGGAG  
 TGGATGCACAAGAGTTGGCCAGAGATCAATCAGGAATCTGGATCTCTGCTGACAAAGACCCAAAGATAAATCACTGA  
 AGCTCGTCCCTTTACGCTCCCTGGGTGGAAGAGTGGACGATGACAAACCTTTGCTCTCTCTGCGAGCTCGACCTCGTGTACTA  
 TTCTTTGTCTGGGCGTTTGCACATGTTTGTGAGATTATGGAAGAACTTTGAGAAGACGCTCTTATCCCAAT  
 AGAACGTCAAGCTCGTGTTTCTGCTTTCAATTTGACTCCAAACCTGACAAGGCCAAACAGTTGAATCATGA  
 GAGATTACCGCATTAAGTACCTTAAAGCCGACATCGAGATTGTGCTGTGTCTGGAGATTTTCAAGACCTTGG  
 CCGTGGAGATGAGTACCTCCAGTTTAAACATGAATCTTTGCTCTCTCTGCGAGCTCGACCTCGTGTACTA  
 CAGAAATCTTTCAGCGATGTCGAGCAAAATACAGTTCTGGGCGAACAATAATTTTCCAACTCACTTCAGCCAGT  
 ATGACCAAAGATTGTTTATGTTGGGAAAGTTCCAGTGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA  
 TCCAAGCTGGGGGCTGGAGGATGTGGACCTTTCAACAAGGTTTCAGGACAGTTTGAAGAGTTTATGAGCC  
 AGGAATAGGAGTAGTCCAGCTCCACCATCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAAGAT  
 GCTTGGGTTCCAAAGCATCGACCTATGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA  
 GTTACAGTAAAAGCAGCAATAATATGGCTCAGTGAGGACAGCCCTATGTCCAGCTTTGCTGGAAAAGACGTTT  
 TAATATATCAATTTTCTTCAAAAATTTTGTGATCAGTTTTTGAAGTCCGTATACAGGATATATTATAC  
 AGATGGTTTCTTACATAGGACTCCTTAAGATTGAGCTTTCTGAACAGAGAGGTGATCAGTTGTGCTTTGAA  
 CAGATCTTCTGCTGAACATTTATGACGACACTGCTTAACCTTTGACITTGACITGATCATGATGAACAAACCTT  
 TTTAAAAAATGTTTCTTTGAGACCTTTGCTCCAGTCTTATGGCAGAAAACGTGAACATCTCCGAAAGAT  
 TATTGATCAAAAGCATGTAATCTGGTAAATGTTCTGTTGATTGTTAATCTCCACAGATTCTACCTTTTGT  
 GTTTGTTTTTTTTTTTTACAAATGTTTAAAGCCATTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA  
 GCTGTTTCATCTGTCTCCAGGAGGCTTCCAGAGTTGATCAITTCCTCATGCTGCTCATGCTGATGCGGCG  
 CAGCTAGGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGAGCGGAGTCTCACTCTGTATCCAGCGGTGAAT  
 CAGTGGCGCAATCTGGCTCACTTTAACTCCACTTCCCTGGTTCAAGCAATCCCTGCTTCCCTCCCGAGT  
 AGCTGGGATACAGGCGACACACCCAGCCAGTCTGTTTGTATTTTATGTAAGAGCGGGGTTCACCAT  
 CGAAGCCAGCTGGCGCACTAGTTTAAAGCAAGGGGCGTGAAGAGGCAGTGAAGTATGGGCTGTCTCG  
 TGGTAGTTTCTTCCGCTTAAATAGACTGGCATTAATTTCAAGAAGGATTGGCATTTCTCTTTCATGACCTT  
 CACTTTAAAGGCTTAAATATTAAATGTTAAGATGACAAAGATGAATTAATCAATAAATCTGATGACAGCACT  
 GAACATACAGCATAACACCTTAATCAAAAGCTTGGGAAAATGTAATGGTTTGTCTTTCATCTGCTGCT  
 TGTATTGTTGGGTTGAGATGTTTTCATCTTTCATCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT  
 TTTATTATATCTGTTGTTGACAGCTCTGCCATTTCTGAGTACCTGTAGTTAGTATTATTATGTGTATCGG  
 GAGTGTGTTTAGTCTGTTTATTTCAGTAAACCGATCTCAAGATTTCTTTTGGAAACGCTTTTCCCTCC



**FIGURE 143B**

TTAATTTTATATCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTGGTGCTCATGTGTTTGGG  
GACAAAAGTGAAATGAATCTGTCTATTATACCAGAAAGTTAAATCTCAGATCAAATGTGCCTTAATAAATTTGTT  
TTCATTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTGTAAATAG  
CCTGATGCTCATTTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCAT  
ATTCCTGTTTtagctGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAAA

4007306.123401

**FIGURE 144**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 91812, pI: 9.52, NX(S/T): 3  
MAARGRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAYRTWSKTI PGKVQFFSSEG  
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLNFLR  
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT  
THEDVEVGRCVRRFAGVQCWWSYEMRQLFYENYEQNKGYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE  
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNPMYGAEYILDLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPEPKDKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGEWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEDDVLFENKVVQAGLKTFRSQEVGVVH  
VHHVPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
 TTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGC  
 ACGGACGACGCC**TATGA**AGCCCTTAGTCCCTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
 CAAGTTTTAGAGAACCTAGTAGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC  
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA  
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAAATACA  
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC  
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGTCATGCAGAGGAACCTTATATTG  
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAAACTGAGGCACCAAGAATG  
 TTGCCAGTTGTTACTGAAATCATCTACAAGTCCATATGTTACCTCATACAAGTACCTGTCA  
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
 CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAAT  
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGA  
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAAACGAAGCC  
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA  
 GTAGGACGAACAAGTAATAAAATTTGATGACATCGAACTGTTATTAAACATGCTGTGTAATTC  
 TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG  
 CTGCTACAGTATTCAATACATTAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
 AAAGTTTAT**TAA**ACAATAATATAAAATTTTAAACCTACTTGATATTCCATAACAAGCTGA  
 TTTAAGCAAAGTGCATTTTTTACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT  
 AAAAAATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTATGTTATGAACA  
 ATTTTCATATGCACTAAAAACCTAATTTAAAAATAAAATTTTGTTTCAGGAAAAA

101706-23101

**FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864  
><subunit 1 of 1, 350 aa, 1 stop  
><MW: 39003, pI: 5.59, NX(S/T): 1  
MKPLVLLVALLLWFPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLTNPIS EETTTFTPTGGFTPEIGKKKHTESTPFWSI  
KPNNVSIVLHAE EPIYENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK  
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNP  
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIE TVINMLCNSRSKL  
YEYLDIKCVPPMEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19

148/249-148/249

**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCCTG  
 ACCTCCAATTCATCCATCCACCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCACACA  
 GGAATATCCATGCGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
 GTGGCAAGTCACTGGACCGGCAAGTTTGTCCAGGCCTTGGTGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCCGTTCTTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
 GTATCGAGGGAGAATCAGTTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTCTAAGGC  
 TAAAAAATCACTCCCTCGGACATCGGCCTGTATGGTGTGTTTTCAGTTCCAGATTTCAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC  
 CCACAGCCAAGTGGAAAGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAAATGCTGGGAGCAT  
 ATTGTGTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAAATCCA  
 GCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCCGAAACACG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTCGCTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACCTGGGAC  
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACATGTG  
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC  
 ATTCAATCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC  
 CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCTATATCCAGCATGCGATGTATGACGA  
 GGAAGGGGGATCCCATATTATATGTCAGTGTCTGGGGATGAGACAGAGAAGACCCTG  
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCCCCGACAGGTGGC  
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCAGCCCCCACTCTCCTTTAGGGAGC  
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT  
 TGGCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGAGCGGAATAGACTCA  
 CATTAGGTTTGTGTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCCTGCCTCAGAGGTGAAGATTAAAGAGA  
 CACGGAATGTGAATCATGCTTCAGGTTTGAGGGCACAGTGTTTGCTAATGATGTGTTTTTA  
 TATTATACATTTTCCACCATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA  
 TACCAATACCCCATGGAATAGTTATGAAACCTGCTTTGTGAGGCTCAAAGAAATAAGAG  
 GAGGTAGGATTTTCTACTGATTCTATAAGCCAGCATTACTGATACCAAAACACGGCAAG  
 AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAA  
 TTCTAAATAAAATTTTAAACAATTAACCTAAACAATATATTTAAAGATGATATATAACTACT  
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAAATTTAAATATCAACCAGTGAATT  
 CAGCACATTAATAAAGTAAAAAGAAAACCATAAAAAATAAAAAA

10017306.123111

**FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866  
><subunit 1 of 1, 466 aa, 1 stop  
><MW: 52279, pI: 6.16, NX(S/T): 2  
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC  
GVVMGMIIVFFKSKGKIQAELDWRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS  
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTTGTGGGAACCCCTGGGTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA  
 TTACTATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT  
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
 TCTCCATTAAAGGAAGAAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
 ATAAAATTGTTCAACTTGTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA  
 GATCCTCACTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG  
 AAGTAGAAGAGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGTCTCACTGTTTTACAACATATAA  
 GAACCCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAACGGG  
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT  
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGCTGACTCTGGAGGACCCTGGTTAGTTCAGATGCTA  
 GAGATATCTGGTACCTTGTCTGGAATAGTGAGCTGGGGAGATGAATGTGGGAAACCAACAG  
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA  
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATACAGAAATGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
 TGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC  
 TTGTTGACATAAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTC  
 AGCTCCTCTCATTTTCAGCAAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTTATTATGAAAGGTCAAGCAAAAGACAGCAGAAATACCAATC  
 ACTTCATCATTTTAGGAAGTATGGGAACAAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
 TCCTTATTTTCATTTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
 ACCTATAATAATTATACAACCTCATGCAATGTACTTGTCTTAAGCAAATTAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

**FIGURE 150**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871  
><subunit 1 of 1, 423 aa, 1 stop  
><MW: 47696, pI: 8.96, NX(S/T): 3  
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD  
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR  
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL  
GQSLRIVGGTEVEEGEPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG  
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDV  
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD  
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)



GTCTGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
CAGCCTGAGATCTTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
CTGCATCAAGGCCATCCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
CGTGACCTTCTTGGTTCACAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAG  
CAGATGAGACTGAGACGGCGTGGCCGCTTTGCCGGCTGTCCCTTGCAGCTACGACCACTGC  
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTTCGGGCCCGCGGCCCTGCCCTGTGCC  
AGGACTCTCCAGCCCCGCGCAGCCGCCGACCCGCGCGCATGGGAGAAGTGCGCATTGGCG  
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGGTCTCTCCACTACTGG  
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCGCTGAACGCTACGGTCCG  
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATATGTCGTTTGCCTAGTGGCCGCTA  
ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGGCTCAGAGGGGGCCGACATC  
CCTGCCTTCGGGCCTTGCAGCCGCTTGGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC  
GGCCGTTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
GCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGACAGGGGCGCT**TCGA**  
AAGGGGCTTCGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCTTGGCCCCG  
GGAAGAGGAAAAACCGCTGCCCTCCAGGAGGGCTGGACGGCGAGCTGGGAGCCAGGCCGAC  
GCTCCAGGGCCACGGCGAGTTCATGTTCTCAGGACTAGAGCCTTGTTTAGGTCCGGTACTT  
GGCGCTTTGTTTCTCGCTGAGGTTCTGGGAAGGAATAGAAGGGGCCCAATTTTTTTTA  
AGCGGCCAGATAATAATAATGTAACCTTTGCCGTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 152**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874  
><subunit 1 of 1, 238 aa, 1 stop  
><MW: 25262, pI: 6.44, NX(S/T): 1  
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE  
LQRVGPAACLCPLGSSPAQPPDPPRMGEVRIAEEGRAVVHWCAPFSPVLHYWLLWDGSEA  
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVQAGGEGLEGADIPAFGPCSRL  
AVPPNPRTLVAHAVGVGTALALLScaalVWHFCLDRDWGCPRRaaARAAGAL

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

100730701

**FIGURE 153**

AGAGAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCCGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCCGGG  
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGGC  
 TTCTCCCTTACGGGGCTCAC**AATG**CCAGAGAAGATTCGTGAAGTGTCTGCCCTGCCTGCT  
 CTACGCCCCCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA  
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTG  
 ATTTTGACTTACTTTCTGTGGTTTATCCGGTCATGATTGCTGTTTGCCTGTTTCTTATCAT  
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCAATGGTACT  
 TTGGAAGTTTGCTTGTCAATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG  
 GAACCTATGGTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTCAGAGAGAGATTTAAGT  
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCCAGAT  
 TCCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAACAGGCCCCCAGGAAAGATCTCAGTGA  
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTGAAGAGAACCAAACTGC  
 AGGTGCTGAGGTTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGAGCCTGGGACAGACCAATGATGTC  
 CTTGAAGATGACAACTCTCAGCACCTGTCAATGTCCCTCAGTAGAACTGTTGAAACCAAGCC  
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG  
 GAGTTA**TAAA**AGAAATGTACAGAAGAAAACCAAACTGTTTTATTGGACTTGTGAATTT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAATAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAGTTTCAATGTCATAAGTCAC  
 CACCTGGACAATAATTTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT  
 CGCATCCATGCAACAGAGTCACATATGGTGGGACTGGAGCCATAGTAAGGTTGATTACTT  
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACCTTTC  
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAATATTCTTACCCTTAAAA  
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGATTTTTTGTATATAAGTCTGTGTTAAA  
 TCTGTATAATTCACTCGATTTCACTTCTGATAATGTTAAGAATAACCATTTATGAAAGGAAA  
 ATTTGTCCTGTATAGCATCATATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT  
 CCTGGGCTTATATTACACATATACTGTTATTTAAACTTAACCACTAATTTGAAAATTA  
 CCAGTGTGATACATAGGAATCATTATTCAAGATGTAGTCTGGTCTTTAGGAAGTATTATAAA  
 GAAAATTTGCACATACTTAGTTGATTCAAGAAAGGACTGTATGCTGTTTTCTCCCAATG  
 AAGACTCTTTTGCACATAAACACTTTTTAAAGGCTTATCTTTGCCCTTCTCAAACAAGAA  
 GCAATAGTCTCCAAGTCAATATAAATCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAAACATGTGACAAATTTAGAGATTTTGTGTTTTTTCACGTGATTA  
 ATATACTGTGGCAAAATACACAGATTATTAATTTTTTTTACAAGAGTATAGTATATTTATTT  
 GAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGATTTTGTGTTTTATTCTCAGAATATGGAA  
 AGAAAATTAATGTGCAATAATATTTTCTAGAGAGTAA

**FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880  
><subunit 1 of 1, 305 aa, 1 stop  
><MW: 35383, pI: 5.99, NX(S/T): 0  
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMDYLNNVLTTLTAETRVEEAVILTYFPV  
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ  
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF  
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL  
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

10077306 123101

[illegible]

**FIGURE 156**

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSQPLNSLDVKPLRKPRIPEMTEFRKVGIPIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFEPGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEATACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNNSGGPCLSGSLVSL
HCLACGKSLKTPRVVGGEEASVDSWPQWQSVIQYDKQHVCVGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSGFSLAVAKIIIEFNPMYPKNDIALMKLQFPPLTFSGTVRPICLPFDF
EELTFPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAVYGEVTEKMMCAPIE
GGVDTCOGDSGGELPMYOSDQVHGVGIVLGGVGGCGGPSTPGVYTKVSAYNLWYINVMWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGACGCGGCATCCCCAGGCTCCAG  
AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATG**GCCCTCCAGCCCTGGGCTGGACCCCTGGAGCCTCTCTGGGCC  
TTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGCCGCGGGGAGGCGGGCAGGGGCCATGCCCA  
GGTCCAGATACTATGACGGGATGAACGTAGGCACTTAGCTTCTTCCACGAGAGGCCCTCAGGATTTTGACA  
CTCTGCTCTGAGTGGTGGTGGAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCTTGGATATCCAGG  
ATCCAGGGTCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA  
AGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGCTCCTGGTTTCTTACAATGTCACCCATCTCTACA  
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG  
AGGACAAGGTCACTGGAGGGAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGCTTGGTGGATG  
GGATGCTCTATTCTGTTACTATGAACAACCTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCGAGC  
CTGTCTCAAGACCGACAACTTCTCCGTGGCTGCATCATGACGCCCTCTTGTGGCAGCCATCCCTTCGACCC  
AGGTCCTCTACTTCTTCTCGAGGAGACGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  
CTAGAGTCTGCAAGAATGACGTGGCGGGCGAAAGCTGCTGCAGAAAGTGGACCCATCTCCTGAAGGCCGACG  
TGCTCTGCAACCCGACCGGGGAGCTGCCCTTCAACGTCATCCGCGACGCGGTCTGCTCCCGCCGATTCTCCCA  
CAGCTCCCCACATCTACGCACTTTCACCTCCAGTGGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCCT  
TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAGAAACTTCACGCTGGACTA  
CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAAGTGTCTGAGTGGGCCCTCCTCTGATAAGGCCCTGACCT  
TCATGAAGGACCACTTCTCTGATGGATGAGCAAGTGGTGGGACGCGCCCTGCTGGTGAATCTGGCGTGGAGTATA  
CACGGCTTGCACTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCCACAG  
GGTCGCTCCACAAGCTGTGTAAAGTGGGACAGCAGTGTCTCATGTTGGAGAGATTACGCTGTTCCTCGACC  
CTGAACCTGTTGCAACCTGACGCTGGCCCCACCCAGGGTGCACTGTTTGTAGGCTTCTCAGGAGGTGTCTGGA  
GGGTGCCCGGCAACCTGATGTGCTATGAGAGCTGTGTGGACTGTCTTCCCGGGACCCCACTGTGCTCT  
GGGACCTGAGTCCGAACTGTGCTCTGCTGCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG  
GGAACCCAGAGTGGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTCGGCCTCAGAGCGCCCGCAAACTATTA  
AAGAAGTCTCGCTGTCCCAACTCCATCTGGAGCTCCCTGCCCCACCTGTCAAGCTTGGCCTCTTATATT  
GGAGTCATGGCCAGCAGCACTCCGAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATGATCAGG  
ATGGAAGTGGGGGTTCTACAGCTCTGGGCACTGAGAATGGCTTTTACATGCTGTGATCTCTACTGGGTGG  
ACAGCCAGGACCAAGCCCTGGCCCTGGATCCTGAAGTGGCAGGCACTCCCCGGGAGCATGTGAAGTCCCGTTGA  
CCAGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTTACTGGCCCACTTTGTCACTGTCACTGTCTCT  
TTGCCTTAGTGCTTTCAGGAGCCCTCATCATCTCTGTGGCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAG  
TTCAGGCTGTGAGACCTGCGCCCTGGGAGAAGGCCCTTAAGCAGAGAGCAACACTCTGACCTCCAGGATCCCAAG  
AATGCAGGACCTCTGCCAGTATGTGGACGCTGACAAACACTGCCTAGGCACTGAGGTAGCT**TAA**ACTTAGGCA  
CAGGCCGGGCTCGGTTGCAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCAGCAGCCTGACTAGGATGACAG  
CAGCACAAAGACCACTTCTCCCTGAGAGAGCTTCTGTACTCTGCACTCACTGATGACACTCAGCAGGGT  
ATGCACAGCAGTCTGCCTCCCCATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC  
CCCCAGACCTGCTCTACACTGATGATGAAGAACTGGAGAGGATCCTCAGTTCTGGCCATTCCAGGACCTC  
CAGAAACACAGTGTTTCAAGAGACCTTAAAAACCTGCCTGTCCAGGACCTTATGTAATGAACACCAACATC  
TAAACATATCATGCTAATGCACTCTCTGGAAACTCCAATCTGAAGCTGCGCTTTGGACACCAACACTCCCT  
TCTCCAGGGTCATGCAGGGATCTGCTCCCTCTGCTTCCCTTACAGTCTGTGACCCGTGACTCCAGGAAGTC  
TTTCTGAAGTCTGACCACTTCTTCTTCTGCTCAGTTGGGGCAGCACTCTGATCCCTTCTGCCCTCCAGGATGG  
CAGGGTAACTGTAGCCTTCTTCACTCCTTTACCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCTTGT  
TTTGGGATTCAGAAACTGCTGTGACAGACTGTATTATTTTATTAATAATTAAGGCTTAAAAAA

**FIGURE 158**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGFMPrVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDNFTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTFLLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPE
NPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSQVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLFDPDEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAPVEASSTVYNGSLLLVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704

101730123101



**FIGURE 159**

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
 TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTGCTC  
 TCAGAGGCTGCCAAAATCTTGACAAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG  
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTTCTTTCTGGAAGAACTTAGG  
 TGGCAGAGGAAAAATTTGAAAACCTATTAAATGTTCTAGAACTACTTGGCGTTGCAGTGCAGTC  
 ATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAAATGAGAAGTTTCGACATGGTGATA  
 GTTGAACCTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGGC  
 CATTTCTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCTTGTCTTATGTTG  
 CAGTATTCGGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCATTAACCTGACTTTGCTCTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTAT  
 GTTGGAGGCTTGATGGAAAAACCTATTAAACAGTACCACAAGACTTGGAGAACTTCATTGC  
 CAAGTTTGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACTGTCA  
 ATCCGGAAATCTTCAAGGAGATGAACAATGCTTGTCTCACTACCCCAAGGGGTGATATGG  
 AAGTGTCAGTGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAAATGTGAAAATGTGGA  
 CTGGCTTCCTCAGAGTGACCTCTGGCTCACCAAGCATCCGCTGTTTTGTCAACCACGGCG  
 GGCAGATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGTTGGGGATCCCTCTCTTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTACAGTT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCCGCGGAGTGGCTGCCAGTGTCTATCTGCGCTCCACCCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGTCTCTCCAGACAGGGGGCGCGACCTCAAGCCCTA  
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGC  
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACAT**TA**AGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
 GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC  
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
 TAATTTTGTCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCTC  
 CTGTGCTCCTTTGTTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
 GACCACTGACCTTCAGATTTCAGCCTTAAATCCACCTCCTTCTCATCGCCTCTCCGAA  
 TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGATATTTCTTTCAGTTTCTGTTT  
 TGTCTCCACATATTTCTTCAATGCTCAGGAAGCCTGCCTGTGCTTGAGAGTTCCAGGGC  
 CGGACACAGGCTCAGAGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAAAATAAAGTTTACA  
 GCGTTATCTCTCCCAACCTACTAA

**FIGURE 160**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169  
>subunit 1 of 1, 523 aa, 1 stop  
>MW: 59581, pI: 8.68, NX(S/T): 1  
MAGQRVLLLVGFLLPGVLLSEAAKILTIISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKRGP  
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF  
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV  
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELEWF  
INSDFAFDFAFRLPLPNTVYVGGIMEKPIKPVQDLENFIKFGDSGFVLVTLGSMVNTCQNP  
EIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ  
NSIMEAIQHGVPVVGIPFLFGDQFENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK  
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPWHEQYLFDVVFVFLGLT  
LGTLWL CGKLLGMAVWWLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTGTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
GCCTCTGGCATATGCACACACTCACACATCTGTGCACACCCGTCACACACATACCATGTT  
CTCCATCCCCCAGGTCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCCTGAAGCTCT  
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCCTTCTCTCCCAAAGCCCA  
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT  
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACGCCAGCCCTAGAGAGGGC  
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA  
AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACTGGC  
TACCAGGTCCCTTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
GGGTGGGCCCAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCTTGGTGGTCTGTGA  
GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC  
GAGTGGCATTGTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
ACCAGTGGGGCCATCTACTTCGACAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC  
CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGCTACAGCTTCCGGTTCCATGTGGTGAAGG  
TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC  
TTTGCCAATGATCCTGACGTGACCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGA  
CCCTGGGGACCGAGTGCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT  
CAAGTTTCTCTGGCTTCTCATCTTCCCTCTCTGAGGACCCCAAGTCTTTCAAGCAAGAAT  
CCAGCCCTGACAACTTTCTTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA  
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCCTTCCACCCACCCACCCCAAGTTACC  
CTCCCAGCCACCTGCTGCATCTGTTCTTCCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
AGAAGGAAGATCTGCACTACTTGTGCGCCTCTGCTCCTCCGGTTCCCCCACCCAGCTTCCT  
GCTCAATGCTGATCAGGACAGGTGGCGCAGGTGAGCCTGCAGGCCCCACAGGAGCCAG  
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCCTGTGAGGAAAGCCAGCATCACGGATC  
TCAGCCAGCACCCGTGAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG  
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
GGCTGTCCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
GGTGAGTGTGTTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC  
CTTTGAAGTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCTCTCTCTCCAGGTCTC  
TCACTGAGTTATCTTCACTGTACCTGTTCACGATATCCCCACTATCTCTCTTCTCTCTGAT  
CTGTGCTGTCTTATCTCTCTCTTAGGCTTCCTATTACCTGGGATTCATGATTCTTCTCT  
CAGACCTCTCCTGCCAGTATGCTAAACCTCCCTCTCTCTTCTTATATCCCGCTGTCCCAT  
GGCCAGCCTGGATGAATCTATCAATAAAACAACCTAGAGAATGGTGTGCTGAGTACACTAT  
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA  
TGTTGCAGAGGAAAATAAATATCAAACTGTATATAAAATTAAAA

10017306-123101

**FIGURE 162**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEFVLLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEG GFD RASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWFPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

**Signal peptide:**

amino acids 1-32

[illegible]

**FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184  
><subunit 1 of 1, 388 aa, 1 stop  
><MW: 43831, pI: 9.64, NX(S/T): 3  
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGGRRS  
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPPHIMGLGAF CNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM  
PGKNAVTLNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGWRWVQKKFQKYIGFA  
PCIFHGRLGFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK  
HKTKEGLPETEVLEVN

**Important features of the protein:****Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

**FIGURE 165**

GGGCGGCGGGATGGGGGCGGGGCGGGGCGCGGCGGCGACTGCTGAGGCCCGGACGCAGGGCCGGGCGGGCCCA  
 GGGCCGAGGAGCGCGGGCGCAGAGCGGGGCGCGGAGGCGACGCGGGGACGCCCGCGCGAGAGAGGTGGCG  
 GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTGTGCTGACCTTGTGCCTTGA  
 CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCTGTAGCAGCGCCATGGGCGCTGTGGCTTCTTGAAGACCCA  
 GTTCGTGCTGCACCTGCTGGTCGGCTTGTCTTCGTGTTGAGTGGTCTGGTCATCAACTTCGTCAGCTGTGCAC  
 GCTGGCGCTCTGGCCGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTACTCTGGAGCCA  
 ACTGGTCATGCTGCTGGATGGTGGTCTCTGCACGGAGTGTACACTGTTACGGAGCAGGCCACGGTAGAGCGCTT  
 TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTTCGAGATCGACTTCTCTGTGGTGGACCATGTGTGA  
 GCGCTTCGGAGTGCTGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC  
 GTGTTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGACCGGGACACCGTGGTGAAGGCTGAG  
 GCGCTGTGGAGTACCCCGAGTACATGTGGTTTCTCTGTACTGGAGGGGACGCGCTTACGGAGACCAAGCA  
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCCGGACCAAGGG  
 CTTACCAACCGCAGTCAAGTGCTCCGGGGGACAGTCGACGCTGTCTATGATGTAACCTGAACTCAGAGGAA  
 CAAGAACCCTGCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGGGAGACATGTGCGTGAGGAGATTCTCTCT  
 GGAAGACATCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAATGTACCAGGAGAAGGACGCGCTCCA  
 GGAGATATATAATCAGAAGGGCATGTTTCAGGGGAGCAGTTAAGCTGCCCGAGGGCCGTGGACCTCTGTAA  
 CTCCTGTCTGGGCCACCATTTCTCTGTCTCCCTCTTCAGTTTGTCTTGGCGCTCTTGGCAGCGGATCACC  
 TCTCTGATCTGACTTCTTGGGTTGTGGGAGCAGCTTCTTTGGAGTTCGATCTTACAGGAGATCGCT  
 TGAACCTGGGAGGTGGAGATTGCATGGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT  
 CAGTCTCAAAAAAAAAAAAAACCAAAATTCGAGAAATTCGAGAGTTGAAGTGTAGTGTACTGACATGAAAA  
 ATTCATAGAGGTGAACAGCAGATTGTAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT  
 TTTCAAGCTAATGAAAAAGATGAAGGAAAAATTAACAGCCTCAGAGACCATGGTGCACCGTCACACAAATCAA  
 CATATGCATGATGAGAGTCCAGAAAGGAGAGAGAGAAAGGCTCAGAAAGATGGCCAAAGCTGATGAAAAACA  
 GTAACCTACCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTCTAT  
 AATCAAGTGTCAATGACAAAGATCTTGAAGCAGCAAGAGATGAGCACTTATCTTGTTCAGAGGATCTTTG  
 ATCAGATTAAACAGCTCATTCTCTCAGAAATCATGGGAGCCAGGAGATGTGGGATGAACACTGTTGAAGGCAA  
 AACCTTCAACTGTAATTAATGGACTTTTGTCTTAGTGTCTGACTGCTGACTCTTGTCTCAGGACAGTTTCTCA  
 ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGTACCTGTAGGAAGGCTGTCTTTAGGCCGGGCACAGTGGC  
 TTACACCTGTAATCCAGCACTTTGGGAGCCAGACGGTGGATCATTTGGGTGAGGCTGATCTCAAACCTCT  
 GAGTTTCAGGTGATCTGCCCGCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCTGGCCGGA  
 ATTTCTTTAAGGCTGAATGATGGGGCCAGGCACGATGGCTCAGCCTGTGATCCCAAGATGATCTGGATTGTA  
 AACATGCACCACCATGCTGGCTAATTTTGTATTTTAGTAGAGACGTGTAGCCAGGCTGGTCTCGATCTCCT  
 GACCTCAAGTGACCACCTGCTCAGCCTCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTGGCCTTGA  
 GCATCTTGTGATGTGCTTATGGCCATTGTATATCTTCTATCTTCTTGGGGAATGTCTGTTCAAGTCCCTTG  
 CCTTTTAAATTTTATTATTTATTTATTTATTTATTTTGAAGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTA  
 CAGTGGGCACAGCTTGGCTCAGTCAGCCTCGACCTCCTGGGCTGCAGTGATCTCCACCTCAGCCTCCCTGTG  
 AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTCAACATGA  
 TGCCAGGGCTGGTCTTGAATCCTGAGCTCAAGTGATCTGCCTGCTCAGCCTCCCAAAGTGTGGGATTACAGA  
 CATGAGCCACTGCACCTGGCAAACTCCCAAATTAACACACACACAAAAAACCACTGATTCAAAATGGGCA  
 GAGGGGCGGGGTGTGGCCCACTGACAGGAGAGTGGAGGAGTGGCTGGGATGAGAAAGTGTGAGGCTG  
 CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACACAGAGTGAGACCTGTCTC

**FIGURE 166**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVSVGLVINQVQLCTLALWVPVSKQLYRRRLNCR LAYSLWSQLV
MLLEWWSCTECTLFDTQATVERFVGKEHAVIILNHNFEIDFLCGWTMCERFVGLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLITFLGFGVGAASFGVRRLLIGESLEPGRWRLQ
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169



GATATTCTTTATTTTTAAGAACTCTGAAGTACTATGCATCACTCCCTCCAATGCTCTGGGGCA  
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGCGAGGCCG  
GCTTACGGCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTCTTAGGATCAA  
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT  
ACATGTGGTGTCTCTTGTCTGTTCTGTTAATGTGGTATGCCATGGGGTCTTTCACAAGCCT  
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCACTACTCTCTCTAATATGTAGTC  
ATCCTGCAGATTTCAATCTTAACATCATTTTCTCCAGGATCTCGGCTGCAGAAATCTCAT  
CTTGTTTAATGCTCTATAAGACCACCTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
TCTTTATGTGCGTTTGTGGTTGTATGGTTGTGTCTGTTCCCAAGATGCCAGCTCTGAGC  
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCTTACATGTGGTGGGTGCT  
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAAGATTGAAATCTCTCAGTTCACCA  
GATGGTGTAGGGCCAGCATTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
TGCAGGTCCTGATTCACTAGGCCAGGTTGGGCATCTTAACAAACTCCCAGTGATGCTGA  
TGCTGGTCCTATGAACATATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAACATGGTGAACCCCATCTGTACTAAAAATACACAAATAGCTG  
GGCATGGTGGGCATAGCTTGTAGTCCCAGTACTTGGGAGGCTGAAGCAAGAGAAATCGCTG  
AACCTGGGAGGCGGAGGTTGAGTCAGGCAGCGAGTCAAGCCACTGTATTCCAACAGGGTGAC  
AGAGTGAGACTCTATGTGCCAAAAA

**FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234  
><subunit 1 of 1, 143 aa, 1 stop  
><MW: 15624, pI: 9.58, NX(S/T): 0  
MHHSLQCPGAATRHHLVCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRRLIRPWVRR  
EGKINFYTNMGDSWGLRPASSVKFLGSAYTFFSLTWHHTLLKASQGFSLFLGSKYLELQEPSWS  
GPCPPGQLHCTCGVLLSFL

**Important features of the protein:****Signal peptide:**

amino acids 1-28

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**FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGCTGGCCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
ATTAAATCTGTTTTTTGTTCTCTTGTAAGTACGCTTTACCTTCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGTTTCTACCCAC  
ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTA  
GCTGCGGCTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTT  
CATAGGCGATGGCTCCCCTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
CCAGGACGGGCCCTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT  
CTAACCTTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCAATTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
GGGAAGGAACTTGTCCAAATTATGGGTGAGAAAGATGGAGGTGTGGGTATCACAAAGG  
ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGCTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCATCACCAG  
CCAGGGGCAGCCGCTGCGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCCCCTCCTCCCTC  
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
GCTCAGTGTTGGCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
AACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCAGGCAAAGGACTGTGTGGCT  
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA  
TCCAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCGGGGTGTGGTGGCCTGTAATG  
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG  
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
GTGTGCCGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
AAAAATAAAAAAGAAATTATGTTATTGTAA

**FIGURE 170**

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWLVLLVLLLP TLKSVFCSLVTSLSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSPKPGTA
SPCWFLAGAVPSPPTVSRLEALTRAVOVAEPFLGSCGFGGGPCPGRRRD
```

Signal peptide:

amino acids 1-15

**FIGURE 171**

GCGGGCCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
 CCGCCGCCTCCTGCCCGCGCC**CATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT  
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCTCTTCTCTGGGGAGGCGGT  
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG  
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
 CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC  
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
 CTGGCCCTGGCCCTGGGCTGCCCGCGGACGGGCGCGTGGTGACCTGCAGGTTGGACGCGCA  
 GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC  
 GGCTGAAGCCCGCCTTGAGACCCCTGGACGAGCTGCTGGCGCGGGCGAGGCCGGCACCTTC  
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC  
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
 GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
**CTAG**GGCTGGCCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
 CCTGAGTTTAAATTGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

**FIGURE 172**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAFAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDRLKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRYIIS
LLPLGDGLTLAFKI
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

[illegible]

**FIGURE 174**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDERG
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLDAQASVSPSE
EENSESSSESEKTSDDQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRREARRRELEARRRREQEEELRRLREQEKEKEKERRRERADRGAEERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEEREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTKRSEGFMSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES
```

**Signal peptide:**

amino acids 1-13

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# FIGURE 175

GTTGGTCTCCTGGATCTTCACTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATATATATTAATTA  
 ACACCATTTGAAAGAGAACTATGTTTTCATCAGCAATGCTAATAAAGATGAAGAACTTAAGCCAGAAAGCCAAAGA  
 TTTTCACTTTTCTCCTGTTGATGATGCTAAGCATGACCATGTTGTTTCTTCAGTCAGCTGGCACTTTGAAGCA  
 AAATATTCGAAGACTCAAGCTAACCTCAAGAACTTGTGCTTTCAATAGCTGTATTCCTTTTGGGTTCATC  
 AGAAGGAGCTGGATTTTCAAACTCTTCTCTAGATGAGGAAAGGAGGAGCTGCTCTTTGGGAGCCAAAGACCAT  
 CTTTCTACTCAGCTGCTGTTGACTTAAACAAAAATTTAAGAAGATTTATGGCCTGCTGCAAAAGGACGGGTGGA  
 ATTATGTAAATAGCTGGGAAGATGCCAATACAGAATGTGCAATTTTCACTCAGAGTACTTCAGCCCTATACAA  
 AACTCATCATATATGTGTGGAAGTGGAGCATTTTCATCCAAATGTGGGTATATTTGATCTGTGGAGTCTACAAGGA  
 GGATATTATATTCAAACTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTGCTCCTCAGCAGCC  
 TTTTGTCTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTTGGCAAAGATACTGCATT  
 CACTCGATCCCTTGGGCTACTCATGACCACCACTACATCAGAAGTACACTTTCAGAGCACTACTGGCTCAATGG  
 AGCAAAATTTATGGAATTTCTTCATACAGACACCTACAATCCAGATGATGATAAAATATATTTCTCTTTTCG  
 TGAATCATCTCAAGAAGGAGTACCTCCGATAAAACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT  
 AGGAGGACAACGAGCCTGATAAACAAAGTGGACGACTTTCTTAAAGCCAGACTGATTTGCTCAATCTCTGGAAG  
 TGATGGGCGAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCCAAGAGATGAAAGAAATCCTGT  
 AGTATATGGAGTCTTTACTACAACGAGTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT  
 CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAATGATGAGGAGAAT  
 TCCTTATCCACGGCTCGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCAGAGATTTTCCAGA  
 TGATGTACCTCAGTTTCTGATAAGCGGCACTCTGTGATGATAAGTCCGTATACCGATTCGAGAGGACCAAGCTT  
 CAGAAGATCAATGTGGATTAACAGACTGACACAGATAGTGGTGGATCATGTCTTCAGCAAGATGGCCAGTACGA  
 TTAATGTTTCTTGGACACAGACTTGAAGTGTCTCAAAGTTCAGCATTTCAAAGGAAAGTGGAAATATGGA  
 AGAGGCTAGTGTGGAGAGTTGCAGATATCAAGCACTCATCAATCATCTTGAACATGGATGTCTCTGAAGCA  
 GCAACAAATGTCAAATTTGGTCCGAGATGGATTAGTTCAGCTCTCTTGCACATGGACACITATTTGGGAAGC  
 TTGCGCAGACTGTTCTTCTGCCAGAGACCCCTACTGTGCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC  
 CTCTAAAGGAGAGCTAGACGGCCAGATGTAATAATATGGCGACCAATCACCAGTGTCTGGGACATCGAAGACG  
 CATTGTCATGAACTGCTGCTGAAGAAAGTGATTTTGGCATTGAATTTAATCAACCTTTCTCGAATGTATACC  
 TAAATCCCAACAGCAACTATTAATGGTATATCCAGAGGTGAGGGATGAGCATCGAGAGGATGTAAGCCCGCA  
 TGAAGAAATCATCAAAACGGAATATGGGCTACTGATTGGAAGTTTGCAAGAAAGGATTCGGGATGTATTACTG  
 CAAAGCCCGAGGACACACTTTCATCCACCCATAGTGAAGTGACTTTGAAATGTCTTGAAGATGAACAGATGGA  
 AAATACCCAGAGGGCGAGAGCATGAGGAGGGCGAGGTCAAGGATCTATTGGCTGAGTCAGCGTTGAGATACAAAGA  
 CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCACTACTGCGAACAGATGTGGCAGAGGAGGAAGCG  
 GAGACAGAGAAACAAAGGGGGCCAAAGTGGAGACATCGAGGAAATGAAGAGAAACGAAATCGAAGACATCA  
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACCTAGTTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC  
 TATAAAAACATTGCTTCTGTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGATGTTTGTCTAAGG  
 CACAAGACAAATATCTGAATAAGACAATATGTGATGAATATAAGAAAGGCCAAAATTCATTTGAACCAAGTTT  
 CCAAGAACAAATCTTGCACAGCAAAAGTATAAGAAATTCCTAAAAATAGGGGGTTTACAGTTGTAATGTCTTTA  
 TGTTTTGAAGTTTGAATTTATTTGTCATGTAATAAGTTGAGCTAAGCAAGGCCCGAATTTGATAGTGATAAGGT  
 GCTTTATCCCTCGAATGTCCATTAAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT  
 CATTTCTTATGAGAACGAGTACCTTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACTCCCATATC  
 AACAGAAAGTCTTTCAGTGAGCCATTCACTCTGGAGAAATGGTATAGAAATTTGGAGAGGTGCATTTATTTCTTTC  
 TGGCCACTGGGTGTAATTTAGTGTACTACAACATTTGATTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT  
 ATTGACTAGTCAGAGTAAACAGGTTACAGAGAGAAGTTGGTCTGATTATGTCTTTTATAGATATATACIAA  
 GCTCTACAGGACAGATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTAATAAAACAAAGGAAACAA  
 TATGATGATATGATCTGATGGGAAGGCATGCAGTGGGATTTGTAGAAGACAGAAGGAACAGAGCCAT  
 AAATTTCTGCTTTGGGGAAAACATCATATCCCATGAAAGGAAGAACAAATCACAATAAAGTGAAGATATGTA  
 TGGAGCTCTTTTCACTGATATATTTCTCTCTTTTAAAAAATATTTATCATCTCTGATATATTTCTTTTACTGC  
 AACTGCTTACCAAAATCTGAGGAACACATAAATCTCTCTGAAGAAATCATAGGAAGAGTAGACATTTATTTATAC  
 ATATGATATTTGATATATATTTCTCTCTTTTAAAAAATATTTATCATCTCTGATATATTTCTTTTACTGC  
 GTTTATTTCTCTCTGATATTTGGATTTGTGATATATTTGATGTAATGAGGAAGAAACCAATATATACACACAGA  
 TAAATGAAGAAATGACATTTCTGGGAGTGGCGATATATATTTGTTGAATACAGAACAGTGTAAATTTTAAAC  
 AACGGAAGGGTTAAATTAACCTCTTGAACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTGTAAT  
 GTAGTATTGTTTGTAAATTAACAAATAAAGCCTGCTACATGT

10017306.123101

**FIGURE 176**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLLLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRCLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYYIRTDISEHYWLNKAKFIGTFF
IPDTYNPDDDKIYFFFRRESSQEGSTSDKTILSRVGRVCKNDVGGQSRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSACVYVSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDVISFIKRHSVMYKSVYPV
AGGPFTFKRINVDYRLTQIVVDHVIAEDGGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEE
LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYKACADCCCLARDEPYCAWDGNA
CSRYAPTskRRARRQDVKYGDPIITQCWDIEDSISHETADEKVIIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHRKRRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT
```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

**FIGURE 177**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAAGCCGACAGGTCATCCTGGAGCATGCCACCGCGGGGAGCAGACA  
CAACTCCCCAGGTCAAGCTGGGAGCAGAGCACTGAAGCTGTTCTTCAGGAGCTGGGTATTTTCCGCCACCCAC  
CTCAGACGTTTCAGCCAGCAGAGGACTGATCAGGTGTGTCTCGGATGGGAGCAGAAAGCGCTGGCTGGCAAGA  
GTGGCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCGTGACTACAAGATCCAGAACCATGGGCAT  
GGGTGAGGTGGGGGGGACAGGTGTGCTGTGCACCTTCTGTCTCAGCAAGAAAGCCTGAGAGAGGGGATCTTGG  
AGCCATTGAGGGTGTCTATGAGCTACAGAGGGGAGGGAAAGGTATTTTAAAGCTAAGCACTGTGGCACAAATAGTTAA  
GAGCACAGTTTTGGAGCTAGACGCACATAGGTTCAAATCTCTCTGTGCTTCTTCTAGTTCTGTAGCCCCAGGT  
AAGGAGTCACTTAACCTCTCTGGAATTCATTTCTCATCACTAAGTAGGGCCAAATATAGCACCCACCTCAT  
AGGAGAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAAGTACCACTAGTAAGTCTATGCCCCACAG  
TATTTCCACCCACCCCTGTTCTCTGCCCTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGGCGCAGCAGGCTT  
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCGGGGACAGGTGAGCC  
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGGCCA  
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGCTGCCAGAGGACCTCTCTC  
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC  
CCCCAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGTGATTTCGCTATCAGGCAGGGCGTGAGGATG  
AGCTGACAATCAGGAGGGTGAGTGGCTGGAGGTATAGAGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
ACCAAGCAGGGCGAGGTAGGCTTTGTCCTGAGCGATATCTCAACTTCCCGACCTTCCCTCCACAGAGCAGCC  
AAGACAGTGAACAATCCCTCGGGGACAGGCCACAGCATCTCTGGCAGAGGCCCTGACAGCTACACCCGACAGA  
GTGCAGAGAGCTGAGCTTCCCTGAGGGGCACTCATCCGTCTGCTGCCCGGGCCAAGATGAGTAGATGAAG  
GCTTCTGAGAGGGGAATTTGGGGGCGTGTGGGCTCTCCCTCCCTGCTGGTGGAGAGGCTCTTGGCCCGC  
CAGGCGACCTGAACCTCTGACCTGAACAGATGCTGCCGTCCCTCTCTCCAGATCTTCCCAACCTGCAC  
CTACCTCTGTGTGGATGGGCCCTCTGACCTGTCTGCTGGGACAAAGCCCTGAGCTTCCCTGGGTTCTGG  
ACATGATGGCACTCTGACTCAGSCGATGCGTCCACCACCTCCCGCGGCTGACCCCGGATCTGCGCAC  
CAGATCCCTCACCCTGAAGCCAGGGAAGCCTTGACCCCGATGTGCTGTCTCTATCTTCAAGCTGTGAGA  
CCACACCATCAATGATCCAGAGCAACACAGCCAAAGCTGGAACTGCCCTTATTTCCACCTCACCCTCAAGGGT  
GGAACTTGCCCTTCCCTTTCTAGAGCTGGAAACCACTCCTTTTTCCTAGTTTGTCTATCATCTTCAAGGAT  
GGAACTACTACCTTCTCTCTGTCATGACCTATCTAGGGTGGTGAATGCTGAAATCTCTGGGGCTGGAAACC  
ATCCATCAAGGTCTTAGTAGTTTGGGCCACCTCTTCCCACTCCCTGGCTCCATGACCCACCCCATCTGGATG  
CCAGGGTCACTGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGGGAAGC  
CTGTAAATGGTCTGAGCGGATTATTGACAATGAATAAGGGACAGAGCCAGGCCAGGGCTGGGCTCTTGTG  
CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACCAAGGGCAGGGGCTGCTCCAGCTGCCAC  
GCTCTATCATATGGAGCAGGTGTTGGSGAAGCGGGGACAGGCTGTTGTCAGGCAGGGGAAGGAGAAGAC  
TGAGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGCTGGAAGTAGAGCTGTGTCCTC  
AGCTGGGGGGAGTGTGCTCAAGTGGAGGGGAGGGCTTCAAGCCACCCACCCCTGGCCCTGCCAGCTGGTAG  
TCCATCAGCAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTGCTTCTCTTCAAGCTGTGTCAGC  
TTTTCCTCGGGCTCCAGGACCTTCCCTACCTCCACCAACCAAGGGATTATAGCAAAGGCTTAAGCCTGC  
AGTTTACTCTGGGGTTTCAGGAGCGGAAAGGCTTAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA  
TTTAGGGCTCAGGCAGACTCACTCACAATCTCCCTGCTGTTGATAGACACTGAGAGAAGGGGAGGGG  
TCAACAATGAGAGCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAGAGGCCACGCCAGTGCG  
AGTCCCGCTGTGTTTTCCTACCTGGTATCAGAAGTGTCTGTTTGGCTGGCCATTGGCTCTTGATGG  
CAGCGCTGGGCTGGGGCCCTCCCTCCGCCCTCAGTGTGGCTCTCAGAAGCTCTGGGGTTCCCTTCAAGT  
CAGCAGGGTTAGGCTGTGCTGCTGAGTCTCCATTCTGTACTGGGGGCTGGCTGAGGCTGGGGCTGGGCC  
TCTCAGGGGGAGCCTCTCATGCGCAGGCATCCCTGCCCTGGGCTGCCCTCCCGACCCCTGACCAACCCCTG  
GGTCTGTGCCCCACAGAGCCGACGCTCCTGTCTGTGGGGAGCATCAGGTTTCTGTGAGGTTCATAGCGCT  
GCTCAATGTGTGTCACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCAACACTCAGAGGCTGTGTT  
GCCCTCCCTCTGACCGAGGCATCTGAGTTTGGTGGCTACTTCCCTCTAGGCTAAGGTAGGGGAGGCTTCTC  
AGATTGTGGGGCACAATTGTGTAGCTGACTTCTGTGGAGCTCCAGTCCAGGAGGAAGAGCCAGGGCCCACT  
TTGGGATCAGGTGCTGTACTGACCTGGGCCCTTACTCCAGCCCTTCCCTGGAGCACTGCCCACTGCCCA  
CAGAGAAGCAGTGGCTCCCTCTGTGGGGGGCGGCTTTTCTCTCTTGGAGGCTCCCTGACGCCAAGTGGAG  
GCTCTTGTGCTGCTGCAATGTGTCAGGGGCTGTCAGAGCCAGGTGCACTGTGATGATGGGAGGGGCTC  
GCTCTGAGGCTGGAGTGGCATCCACACTGGACAGCAGGAGGGGAGTGGAGTAACTTTCCATTCCCT  
TCATGTTTGTGTTCTTACGTTCTTTCAGCATGCTCTTAAACCCAGAGCCCAATTTCCCAAGCCCATTT  
TTTCTGTCTTATCTAATAACTCAATATTAG

**FIGURE 178**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFVRYQAGREDELTITTEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESQSDSDNPCGAEPATAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPAPPTSVLDGPPAPVLPDGLKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

**FIGURE 179A**

CACAGGGAGACCCACAGACACATATGACGAGAGAGACAGAGGAGGAAGAGACAGAGACAAGGCCACAGCGGAA  
 GAGGGCAGAGACAGGGCGAGGACAGAGCGGCCGACAGACAGAGTCTCTACAGAGGGAGAGGCCACAGAGAGCTGCGA  
 AGACACAGGCGAGGAGAGACAAAGATCCAGGAAAGGAGGCTCAGGAGGAGAGTTTGAGAGAGCCAGACCCCTGG  
 GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTCTCTTAAACGGTCTCAGCCCTCTCGAAACCTTTGGC  
 TCTGACCTTTGGCAGGAGTCCAGGCCCAAGGCTACAGAGAGGAGCTTTCAAAGAGTATAGGTTGTGGAGGACTTGGT  
 GCGCTAGACGGCTCAGTCCCTCCAGGCTGCAGTACCAAGTGCCATGCTCCCAAGACGGCTCGCATCCCGGGAGGG  
 CTGTGGACGGCGCTGGCTGTGGGGAGGCCAACCTTGCCTCTGCTCCCATTTGTGCCCTCTCTGCTGGTGTG  
 GCTGCTTTCTGCTACTGCTGGCTCTCTCTGCTCCCTCAAGCCGCTGGCCAGCCCTCCCGGGAGGAGGAGAT  
 CGTCTTCCAGAGAGCTCAACGGCAGCGTCTGCTGCTGGTCTGGCGCCCTGCCAGGCTTTGTGCGCTTGA  
 GGCTTTGGGGAGAGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGCGAGGGGCTGACAGTGCAGTA  
 CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCCACATCAATGGAGATCC  
 GGAGTCGGTGGCATCTCTGCATGGGATGGGGGAGCCCTGTTAGGCGTGTACAAATATCGGGGGGCTGAACATCCA  
 CCTCCAGGCCCTGGAGGGAGGCCACCCCTAACTCTGCTGGGGACCTGGGGCTCACATCTACGCCGGAAGAGTCC  
 TGGCAGCGGTCAAGTCCCATGTGCAACGTCAAGGCTCCTCTTGAAGAGCCCAAGCCCAAGACCCGGAAGGCCAA  
 GCGCTTTGGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAAGATGGCCGCTTCCACGGTGC  
 GGGGCTAAAGCGCTACCTGCTAAAGACTGATGGCAGCAGCAGGAGGCTTCAAGCACCAGAGCATCCGCAATCC  
 TGTCAAGCTTGGTGGTGAATCGGCTAGTGAATCTGGGGTCAGGCGAGGAGGGGGCCCAAGTGGGGCCAGTGTCTG  
 CCAGACCTTGGCAGACTTCTGCTGAGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCTGGGCGCTTGACCATTTGA  
 CAGAGCACTTCTGTTTAACTGCTGAGGCTGTGTGGAGTCTCCACTTGCAGACGCTGGGTGGGTGATGTGGG  
 CACCGCTGTGAACCCGGCTCGAGGCTGTGCCATTTGTGGAGGTGATGGGCTCAGCTTGAAGCTTCACTGTGCTCA  
 TGAACCTGGGTCACTGTCTTCAACATGCTCCATGACAACTCCAAGCCATGCATCAGTTTCAATGGGCTTTTGAGAC  
 CTCTGCCATGTCTATGGCCCGTGTAGTGGCTCATGTGGATCTTGAGGAGCCCTGTGCCCCCTGCAGTGGCCGCT  
 CATCACTGACTTCTGCGAATGGCTATGGCACTGTCTCTAGACAACACAGAGCTCCTATTCGCTGCTGCTG  
 GACTTTCCCTGGCAAGACTATGATGCTGACCGCCAGTGGCCAGCTGACCTTGGGCGGCACTCAGCCCATTTGCC  
 ACAGCTGGCGCGGCTGTGCTGCTGCTGCTGGTCTGCTGGCCACTCATATGGCCATGCCATGTGCGACCAACAA  
 CTGGCCCTGGGCCCTGATGGACACCTCGGGGCCCGCACAGGCTGCATGGGTGGTCTGCTGCTCCACATGGACA  
 GCTCCAGGACTCAATATCCACAGGCTGGTGGCTGGGGTCTTGGGAGCATTGGGGTGAATGCTGCTCTCGGACCTG  
 TGGGGTGGTGTGCTCAGTTCTCTCCGAGACTGACAGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG  
 CCGCGGTACCGGCTTCGCTCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
 GTGTGCTGCTTACAACACCGCAGCCGACCTTCAAGAGCTTCCAGGGCCATGGACTGGGTCTCTCGCTACAC  
 AGGCGTGGCCCCCAGGAGCCAGTGCAAACTCACCTGCCAGGCGCGGCGCACTGGGCTACTACTATGTGCTGAGGC  
 ACGGCTGGTAGATGGGACCCCTGTTCCCCGGACAGCTCTCGGCTGTGTCCAGGGCCAGTGATCATGCTGG  
 CTGTGATGCATATTTGGCTCCAAGAAGAAGTTGACAAGTGATGGTGTGCGGAGGGGAGCGGTTGTGTTGCGAG  
 CAAGCAGTCAGGCTCCTTCAGGAATTCAGGTCAGGGATACAACAATGTGGTCACTATCCCCCGGGGGCCACCA  
 CATTTCTTGTCCGGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAAGTGGCAGATGCTCCTTA  
 TGCCTCAATGGTGAATACAGCTGATGGCCCTCCCCACAGATGTGTAAGTCTGCTGGGACAGCTCAGCTTGGGCTA  
 CAGCGGGGCCACTGCAGCTCAGAGACACTGTGAGGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTCT  
 AGTGGCTGGCAACCCCGCAGACAGCCCTCCGATACAGCTTCTCTGCTGGCCGCGCCGACCCCTTCAACGCCACG  
 CCCCCTCCCCAGGACTGGCTGCACCGAAGACAGATTTGGAGATCTCTCGGCGCGCCCTGGCGGGGACG  
 GAAATGAACCTCACTATCCCGGCTGCCCTTCTGGGACCGGGGCTCGGACTTGTGCGGAGAAGAGAGAGCTT  
 CTGTTGCTGCTCATGCTTAAGACTCAGTGGGAGGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT  
 GCGCAGGCTGGCCCTGCCCTGGTTTCTGCTCGTGGGAGCGAGTATGGGTTAGTGGATGGAGGGGCTGACAGAC  
 AGGCCCTCCATCTAACTGCCCTCTGCTGCTGCGGCTCAGAGGAGGAGGGGGAAGGCGAGGGGCGCTGGGCC  
 CAGTTGATTTATTATTAGTATTATTACTCTTTATTAGCAACAGGAAGGGGACAAGGACTAGGCTCTCTGGGAA  
 CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGT  
 TGTGTATCGGTGTGTGTGTGTGTGGAAATGTGTGTGTGCTTATGATGATGACAACTGTTCTGTCTGTTCTCT  
 TCTCTGAATTTATTTTTGGGAAAGAAAGTCAAGGGTATAGGTTGGGCTTCAAGGAGTGAGGGATATCTTTT  
 TTTTCTTTCTTTCTTTCTTTCTTTTCTTTTGTGAGACAGATCTGCTGCGCCAGTCTGCGGAGGTGCAATG  
 GCACAACTCTCGGCTCAGTGCATCTCCCGCTCCCGGGTTCAAGTGATTTCTCATGCTCAGCCTCCTGATAGCT  
 GGATTAAGGCTCTGCTGCGCCAGCCCGCAGCTAATTTTGTGTTTGTGTTGGAGACAGATCTGCTGATGTGTC  
 ACCAGGGCTGGAATGATTTCAGCTCACTGCAACCTTGCCCACTGGGTTCCAGCAATCTCTGCTCAGCCTCC  
 CGAGTAGCTGAGATTATAGCACTTACCACACCGCCGCTAATTTTGTATTTTGTAGTAGAGCGGGTTTCACT  
 CATGTTGGCCAGGCTGGTCTGCACTCTGACCTTAGGTGATCCACTGCTCTCATCTCCCAAGGTGCTGGGATTA  
 CAGGGCTGAGCAGCCGCTGGCCACCGCCCACTAATTTTGTATTTTGTAGTAGAGGCTTTCAACTGT  
 TGGCCAGGCTGCTTGAAGCTCTGACCTCAGGTAACTGACCTGCTCGGCTCCCAAGGTGCTGGGATTA  
 TGTGAGCCACACCGCCGGTACATATTTTAAATTTGAATTTACTATTTATGTGATCCTTTTGGAGTCAGACAG

**FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCCTGAGCATTAGATTTCATTTGCCAATAATAATACCTCCCTTAGAAG  
TTTGTGTGAGGATTAAATAATGTAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAGGAAA

10017306.123101



**FIGURE 181**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**  
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT  
 AATTGTCCTGTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG  
 ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAATGCACGACTT  
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
 TTAAAGTGATTCTGAATTTTCTGAACCAAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
 TTTTCTTAAAAATCCAAAATCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
 CCTGCCAACGAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAAGTTCCAATAAATGACTATACTG  
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC  
 GCATGCTGGGGAGGGTCT**TA**ATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT  
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT  
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
 AAAAAAAAAAAAAAAAAA



**FIGURE 182**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 37130, pI: 5.18, NX(S/T): 3  
MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTTLIVLFWGSKHFWPEVPPKAY  
DMEHTFYFNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIIYFVGLQKCFIKT  
QIKVIEPFSEPEEEIDENEEITTTFFEQSVIWWVPAEKPIENRDFLKNSKILEICDNVTMYWI  
NPTLISVSSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY  
TENGIEFDPMLDERGYCCIIYCRRGNRYCRRVCEPLLGYYPPYCYQGGRVICRVIMPCNWWV  
ARMLGRV

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAAC TGCTCCGGCTGGCACCTGAGGAGCGCGTGACCCCGAGGGCCAGGGAGCTGCC  
 CGGCTGGCCTAGGCAGGCAGCCGACCATGGCCAGCAGCGCCGTGCAGCTTCTGGGCTTCCT  
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
 GCGCCTGCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
 GGCACCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC  
 CAGGGCCACCACGACCAGTGCAAAACACGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTACAGGTGAACGACTACGTG  
TGAGTCCCCACAGCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
 AATGGAGGCAGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATATATATAT  
 TTATGTGGGTGATTTGATAACAAGTTTAAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
 TGGTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAA

**FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSSLIGGTLCLSCQ  
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

**FIGURE 185**

GAGTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
CAGGCGGCAGGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCT  
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCC  
AGGACCTGTACGACAAACCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
GTGAGGCAGAGTTTCAGGCTTCACCGAATGCAGGCCCTATTTCACCATCCTGGGACTTCCAGC  
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCCTCC  
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTTGCCAAAGCC  
AACATGACATGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
GTCTGTGTTTGCCAACATGCTGGTGACTTAACCTCTGGATGCTCCACAGCTAACATGTACACCG  
GCATGGGTGGGATGGTGACAGCTGTTAGACACAGGTACACATTTGGTGCGGCTCTGTTCCGTG  
GGCTGGGTGCTGGAGGCCTCACATAATTGGGGGTGTGATGATGTGCATCGCCTGCGGGGG  
CCTGGCACCAAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG  
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCACACCACCAACAAAGAG  
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCTTCCAAGCAGCACTA  
TGTGTAAAGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAA  
AACAAGGAGATCCCATCTAGATTCTTCTTGTCTTTGACTCAGAGTGAAGTTAGAAAAAGC  
CTCGATTTTATCTTTGGAGAGGCCAATGTCTTAGCCCTCAGTCTCTGTCTCTAAATATCC  
ACCATAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGTCAACATTTTCAATCCTCTAT  
TCTTTTTTTTAAATATAAATTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC  
ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCTTAGTCAATAAACCCATTGATGATCTA  
TTTCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAGAGTAGACCCAAAGATGTTATTTT  
CTGCTGTTTGAATTTGTCTCCCCACCTTTTCACTTTGCTAGTAAATACACATCTACTGAGAA  
GAGCAATTAAGAGAAAGATATTTGTAATCTCTCAGCCCATGATATCTCGGTTTCTTACACTG  
TGATCTTAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTCTACTG  
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG  
TCCTCTTCTGTGCGGGGTACAGAAATGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT  
TTAAGTCTTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA  
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT  
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC  
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCACAGAAGTTCGAGACTAGCCTG  
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG  
AGGTTGGGGCTGACAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
TCTGCTCTAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA  
ACTAATCTTTTAA

**FIGURE 186**

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
>>subunit 1 of 1, 261 aa, 1 stop
>>MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSIGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTQVTRYTFGAALFVGWVAGGLTL
IGGVMPSCIACRDGLAPEETNYKAVSYSHSGHSVAYKPGGFKASTGFGSNTKNNKIYDGGARTE
DEVOSYMSCKHGLDYV
```

**Signal peptide:**

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

### FIGURE 187

GGGAAAACTGTTCTCTTCTGTGGGCACAGAGAACCTGCTTCAAAGCAGAAGTAGCAGTCCG  
GAGTCCAGCTGGCTAAAACTCATCCAGAGGATAAATGGCAACCCATGCCTTAGAAATCGTG  
GGCTGTTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCTATGCCTCAGTGG  
AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG  
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCTTT  
TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTGGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
GTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCT  
GATTGTGTGGAGAGCTCTGTTCTGCTGCTTTTTTGTGTGAACGAAAAGAGCAGTAGCTACA  
GATCTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACGGGAAGAAGATCACCG  
AGCGTCTACTCAGAAGTCAGATGTGTAGTTGTGTGTTTTTTTTAACTTTACTATAAAGC  
CATGCAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAGAAACTTTGATTTA  
CTGTTCTTTAACTGCCTAATCTTAATTACAGGAACGTGCATCAGCTATTTATGATTCTATAA  
GCTATTTTACGAGAATGAGATATTTAAACCAATGCTTTGATTGTTCTAGAAAAGTATAGTAAT  
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTACTTCAAATGACATTGCT  
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG  
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGCTCTCCATTTATAATGA  
AGATTAATAATGAAGGCTTTAATCAGCATTGTAAGGAAATTGAATGGCTTTCTGATATGCTG  
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTCTTTATCCTCTTCTCCAGAGGCTTTTTTT  
TTCTGTGTATTAAATTAACATTTTAAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA  
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
GTTTTAGGAAAGTGAAAAATTTTTGTTTTGTATTGGAAGAAGATGATGCATTTTGACAA  
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTCAATTGCTTACCAAAAAACAACA  
ACAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAATTG  
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTACCAATTCTGTTTAGTTTTACTAAA  
ATCTGTAATCTGATTAATTTTTCTGTTTATTCAAATTTGATGAACTGACAATCCAATTTGA  
AAGTTGTGTGACGCTGCTGTAGCTTTAAATGAATGTCTTATTGCTTTTATACATTTATA  
TTAATAAATTTGTACATTTTTCTAATT

**FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735  
><subunit 1 of 1, 225 aa, 1 stop  
><MW: 24845, pI: 9.07, NX(S/T): 0  
MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLLIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

TCGCC**ATG**CCCTCTGCCGAATGCAGATCCTGGGAGTCGCTCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTTCATCGGCAACAGCAT  
CGTGGTGGCCAGGTGGTGTGGGAGGGCCCTGTGGATGTCTCTGCTGGTGCAGAGACCGGCC  
AGATGCAGTGCAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTTCGGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTACCTCTGGGA  
TTGTCTTTGTCTATCTCAGGGGTCTTGACGCTAATCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAAGGGGAGCTGGGGGCTCCCT  
CTACTTTGGCTGGCGGCCCTCAGGCGCTTTGTGTGCTGGGTGGGGGCTTGTCTGTCTGCACCT  
GCCCTTCGGGGGGGTCCAGGGCCCGAGCCATTACATGAGCGCCGCTACTCAACATCTGCCCT  
GCCATCTCTCGGGGGGCCCTCTGAGTACCTACCAAGAATTACGCTCT**GCA**GCTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT  
CGTACCTTTTGTTTCTGCCTCCTGCTATTTTTCTTTTACTGAGGATATTTAAAATTCATTT  
GAAA**AA**CTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC  
CAGTCAAGCTATGGA**AA**CTAATGCGGAGGCTGCTTGTGTGCTGGCTTTGCAACAGACAGAC  
TGTC**CCCA**AGAGTTCTCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTTCA**CC**CTGGAAAAACAATCATCTG  
TTA**CA**CAAAGGACTGCCACCTCCGGA**AA**CTTCTGACCTCTGTTTCTCCGCTCCTGATAAGCG  
TCCACCCCTCAGGGCCAGGTCC**CA**GCTATGTAGACCCCGCC**CC**CACTCCAACACTGCAC  
CTTCTGGCCCTGCCCCCTCGTCTCACC**CC**CTTCACTACATTTTTATCAAATAAGCATG  
TTTTGTTAGTGCA



**FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIIVVAQVVWEGLMSCVVQSTGQM
QCKVYDSSLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGLASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPGSHMARYSTSAPAIRGPGSEYPTKNYV
```

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
 AGCATCTTCTACCACTCCGAATTGAACCACTCTTCAAAGTAAAGGCAATGGCATTATTTATCCC  
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTGGCATGGTGGGACTCTTGCCACAACCCT  
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
 TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
 TAGCTCCTTGTGGCTCTCCCGCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG  
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
 GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACTTACAGGAGTCTCTTCATCCTGAC  
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
 AGCGCTGCTGCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA  
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA  
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTGGCTCCAAGT  
 ATGGACTATGGTCAATGTTTTTTATAAAGTCTTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
 GAACCTGCTTTATGTCTAGATTACATTGATACGAAAGTTTTCAATTTGTTACTGGTGGTAGG  
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
 TGTACAATGATGGACTACTTATTACTTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
 GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

**FIGURE 192**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDfYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

**Important features of the protein:****Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**CATG**AAGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACCTACCAGTTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

101730673104

**FIGURE 194**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVYFCSSSEASLSPKKVDCSIYKKYPVVAIPCFITYLPVCGSDYITYGN  
ECHLCTESLKSNGRVQFLHDGSC

**Signal peptide:**

amino acids 1-19

**FIGURE 195**

CCCGCGCCCGGTTCTCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC  
CGCGGCCATGGCTGCTCCTCCCGCGCGGCTGCTGTCTTGCCCTGACCGGGCTGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGAAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAACCTAAGACTAAAGTGGCCGTTGATGAGATAAAGCCAAAGA  
ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT  
TCTTCATGTATCTCTTAATGCCTTACACTACTTGTTTCTGATTTCGCTATTTCAGCAGAT  
CTTTTCTACCTACTTTTGTGTATCACTAAGGAAGAGTTAAAAACACATGCTAATGCCTT  
TGATATTTCATGGGAATGCCCTCATTTAAAAATAGAAATAAAGCATTTTGTTTAAAAAGA

**FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742  
><subunit 1 of 1, 148 aa, 1 stop  
><MW: 17183, pI: 8.77, NX(S/T): 0  
MAASPARPAVLALTGLALLLLCWGPGGISGNKLKMLQKREAPVPTKTKVAVDENKAKEFL  
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYD  
EDSAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

1007346-22101

**FIGURE 197**

CGGCTCGAGCCCGCCGGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGTGGGTGATGAGGTGAC  
CGTCCTTTTCTCGGTGCTTGCTTGCCTTCTGGTGCTGGCCCTTGCTCTGGGTCTCAACGCACA  
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTGAGGACCCCAACGCCATCCCAGCCCCAGC  
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT  
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG  
CCCCGGACTCCCCGAGGAGCCCCCTGTGCTACGGCTGAAATTCTCTAATGATTGAGAGCAG  
GTGGCCAGGGCTGGCCCCACGACACCATTTGGCTCTTGAAAAGGACCCAGTTTCCC GGCCG  
GGAAACAGCAGGTGCGACTCATCTACCAAGGCGAGCTGCGTAGGCAGCAGCACCAGACCTTGG  
GCAGCCTTTCACCTCCCTTCCCTCACTGCGGTTCTCCACTGCCAGCTGTGTCACGAGAGTTCGTCCC  
CCAAATCCCCCTGCCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAATTCGGCAGCCT  
GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
CCTTCTTTCCCTGACCGCCACTCTGGGCTTGGCCGGCTTACCCTGCTCCTCAGTCTCCTG  
GCCTTTGCATGTACCGCCCGTAGTGCCCTCCGCGGGCGCTTGGCAGCGTCGCGGCCCTTC  
GGACCTTGCTCCCGCGCCGCGGGGAGCTGCTGCCTGCCAGGCCCGCTCTCCGGCTG  
CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG  
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA  
CTGGGAGTGGGCTCCTCGGGTGCGGCATCTGCTGTGCTGCTGCTCGGCCCGGGCAGAGCCG  
GGCCGCCCCGGGGGCCCTTTAGTGTTCTGCCGGAGGACCAGCCGCCCTCCAATCCCTGAC  
AGCTCATTGGGCTGAGTTGGGACGCCAGGTGCGTGGGAGGCTGGTGAAGGGGAGCGGGAG  
GGGCAGGAGAGTTCCCGGAACCCGTGCAGATTAAGTAACGTGTGAAGTTTTAAAAAAAAA  
AAAAAAA



**FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCV LHCHVSTRVGPPNPCCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

GAGATTGGAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
 ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCCTAAGAACCATCAGCCC  
 TCAGCTGCACCTCCTCCCTCCAAGG**ATG**ACAAAGGCGCTACTCATCTATTTGGTCAGCAGC  
 TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCAGGTGCTGCAGCT  
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG  
 AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC  
 TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA  
 CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA  
 TTGTGTCCGGAGCACGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG  
 CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGAT**TGA**AACAGGTTGCGGGTGCAACCGTGG  
 AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA  
 CTTTCATGTTATTTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAA  
 TGGTTTCTTGGCTTCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT  
 TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNPNL LAGIHC AKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

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**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTACAGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCAGACACCTTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACCTGAG  
 CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAAACCGGGTTAAAGGGAGGGAAGCAATTC  
 AATTTGAAGTCCTGTGAATGGGCTTTCAGAAGGCAATTAAGAAATCCACTCAGAGAGGAC  
 TTGGGGTGAACCTTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAGCAGGCTTGCACACGCT  
 TGTTGGCAAATGT CAGGACCAAGTTAAGTGACTGGCAGAAAACTTCAGGTGGAACAAGCA  
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGAGAAAGCTAACTTGAACATGAC  
 CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCTCTAAGGAAGCGATACAGGCACAGACCATG  
 CAGACTCCAGTTCCCTCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT  
 TGCACCCCTCCCCACCACACCTGCACAGACTGTACAGCCCCAAGCCAGCAAGCACAGCCCT  
 GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATGGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC  
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAAGGAACAGAGCCAGGGCAGGAGAGGTGGG  
 AGCTACCGCCTCATCAAGCAGCCAGGAGGCGAGGATAGGAAGCCCCAAAGAGGGACTGGGG  
 GGCTGATGAGGACGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTCAGCTGGACCCAC  
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCGAGGTGCGG  
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCTGCCACAGCCAGCGTCACTCCTGTG  
 TTTCCATGATGAGGCTTGGTCCATCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
 CCAGGGCCTTCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGCAACTCAAG  
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
 TCATGGATGCCCCACTGCGAGTGGCACCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
 TTACCCCTCAAAGSACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTCCACTGGGAAC  
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGGCCCTGTG  
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAACACTGGAGCGTATGACTC  
 TCTTATGTGCTGCGAGGTGGTGAAAACTCGAACTGTCTTTCAAGGCCCTGGCTCTGTGGTG  
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT  
 TCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG  
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCTTCTCCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTTGCACTGCAAGGAGACTGGGTGTGTCGACATCTCCACTGG  
 TTTCTGGCTAAATGTCTACCTGAGCTGTACCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAAGGGACATCTGGGCT  
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACTGCAGCACACAGC  
 AGGAAGGAGATTCACCTTTGGCAGCCACAGCACCTGTGCTTTGCTGTACGGCAGGACAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG  
 AGAATGGGATGATTGCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAGAAAAA  
 AATAAAGATTTGTACTCGCTCGGTGTGATGGAAAGCCCGCAGAGCTGGCGATTGACCA  
 GATAAATGCTGTGGATGAACGATGATGTCAATGTGAGAAGGAAAGAGAAATTTGGCCATC  
 AAAATCCAGCTCCAAGTGAAGCTAAAGAGCTTATATTTTCAAGACTGATCTTGTGTG  
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAGAATATAGGAAGTTTCTCCTTT  
 TCACACCTTATTTCATTGACTGCTGGCTGCTTA

10017306.423104  
 10017306.423104

**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760  
><subunit 1 of 1, 639 aa, 1 stop  
><MW: 73063, pI: 6.84, NX(S/T): 2  
MLLRKRYRHRPCRLQLLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEYESPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR  
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAF LKEIILVDDLSQQGQLKSALSEYVAR  
LEGVKLLRSNKR LGAIRARMLGATRATGDVLVFM DAHCECHPGWLEPLLSRIAGDRSRVVS P  
VIDVIDWKT FQYYPSKDLQRGVLDWK LDFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAM D  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGG SVEILPCSRVGH IYQNQDSHSP LDQEATL  
RNRVRIAETWLG SFKETFYKHSPEAFSLSKAEKPDCMERLQLQRR LGCRTFWHFLANVY PEL  
YPSEPRPSFSGKLHNTGLGLCAD CQAEGDILGCPMVLAPCSDSRQQYLQHTSRKEIHFGSP  
QHLCFAVRQEQVILQNCTEEGLAIHQQH WDFQENGMIVHILSGKCM EAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTCACAGCTGAGGAAGACCTCAGACATGGA  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTTC  
 TGCCCTCCACACGCTGTCTAGGGCTCTTCATCCTCCCTCGAACCCACAGCCCCAGCC  
 CGCCCCCTGTGTCCAGGGGAGGCCCTCGGCCACAGTCATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGGCAAGTCTGCTGGCACTG  
 CACCCCCAGCCACCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTTGCAGCCCTCATGGCTCGCAACCCCACTCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGACACCTGCCACCCCTGCGGCCATT  
 CTGTTGCGGGGCGGTGGGGAAGGTGTGGACCCCAAGCTCTATGTGACAATTACCATCTCCAT  
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGAGCCAGAAGC  
 GACGCAGACCTCAGGCGAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACGTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCC  
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CCTTCCAGTTGAACCGGTGAGGGGAGGGGCAATGGGATGGGAGGGCAAGAGGGAAGGCAAC  
 TTAGGCTCTCAGAGCTGGGGTGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC  
 CTCCCAAGCCCTGCGCCCTCCCAAGGGGGCTGGACCAAGCTCCTCTCTGGGAGGCCCTTCT  
 CTTCTCCAGTCTCTCAGGATCTGTGTCTTATCTCTGCTGCCATAACTCCAACCTGTCCT  
 TCTTTGGTTTTTTTCTCATGCCACCTGTCTAAGACAACCTGCCCCCTTAACTTGATTCCC  
 CCTCTTTGTCTTGAACCTCCCTTCTATTCTGGCCTACCCCTTGCTTCTGACTGTGCCCTT  
 TCCCTCTTCTCTCAGGATTCCTCTGGTGAATCTGTGATGCCCCCAATGTGGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCTGGCTCCTGCCCTTGACACACCCGGGAACACTCCCCAGCC  
 CCACGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC  
 AGGCCATTTGCACACGCTCCTGCACCTCTCCCCGTCCATACCGTCCGCTCAGCTGACTGT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACTTGTGTCTCAGCTCACTCAG  
 TGGTCAGCGTTTCTGCACTTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGG  
 TGTGCGGCGTCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGAGCCCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTGATGG  
 TCTCGTCCCATTTCCACCATTTGTTTCTCTGCTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCCCAGACTTCAACCCAGCCCCA  
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA  
 AGGGACTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTGTCTGCTGGCTG  
 TCTGTGTGTGGCAATTCCTGGACTTCAGAGCCCCCTGAGCCAGTCCCTCCCTTCCAGCCT  
 CCCTTTGGGCTCCTTAACCTCACCTAGGCTGCCAGGACCGGATCAGTCAGTGTGTTCAAGCC  
 ATCGGAGCTCTGCCCTCAAGTCTACCTTCCCTTCCCGACTCCCTCTGTCCTTCCCTTT  
 CTTCCCTCTTCTTCCACTCTCCTTTGCTTCCCTGCTTCCCTTCCCTTCCCTTCCCTCAGGTT  
 CTTCCCTCTTCTCACTGGTTTTTCCACCTTCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT  
 GTGATATATATTTTTGTATTATCTTTCTTCTTCTGTGGTGATCATCTTGAATTACTGTG  
 GGATGTAAGTTTCAAATTTTCAAATAAGCCTTTGCAAGATA

1007306.12301

**FIGURE 204**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGSLPIEAIIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 205**

GTTAACACAGCGCAGTCTCTCGTGCCTCCCGCCGCCGCTGCCCTCACTCCCGGCCAGGATCG  
CATCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACAGCTGTGGAACAGAGCCGGCGAGCTGCC  
GTCGGGAGAAGGCCCCCGTGGAGAGACCAAGCCCCGCCGGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCCACCCTGCGGCCAGGACCCGAGGACAGCACCCGCGCAGGAGCGGCTGGACCAGGGC  
CGCGGGTGCCTGGGGCCCGGCGCTATCGCGGCATCTGATCGCCGCCCTCTGGCCACCTG  
GCTGGTGTCTGGCGCTCGTGTGCTCGCGCTGAGAAAGTTTCTGCCTCTTGAAGCGAATAAA  
GGGGCCCGCGCCGCCCGCGCGCTCGGCAAAAAA



**FIGURE 206**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG  
 CGGGCCGGGACGGGCA**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
 ACTTCAAGTCCTGGTGGGTGGGCGACATCCCGTGTGAGGGGCGCTGCTACCGACTGGAGC  
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATACCCGGGAGAAGCTGGA  
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
 CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
 ACCGAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGGACCTCCCC**TAAG**TAGCCC  
 CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
 GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACATACATGAAAACCAAGGCCGAT  
 CGACTGTGACGACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACGTGACAG  
 ACTCGCACGTCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCACCCGT  
 GCCAGGGCCCTACTGTCCCTGGGGTCCAGGCTCTCCCTGGAGGGGGCTCCCCGCCTTCCAC  
 CTGGCTGTATCGGGTAGGGCGGGGCGGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGT  
 CCCACAGGTCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCTGAACACATAAAATAAC  
 TGGCACAAGTAAGTCCCTCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGTG  
 GGTGAGTATGTGTGGGCGACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGCTCCCGA  
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCTTTTCTCCCTCAAAG  
 GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTCCCTAAAGGGTCCCCATAGGGTCTGGTTCC  
 ACCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCTACGATGGTTAGGGGTGCCCC  
 ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGCCGC  
 CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT  
 AGATCAGTGGGGGCATGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
 CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
 CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCGCTCGGGAGA  
 AGGGGTGCTCGTAAGCCAACACAGCGTGCCGCGCCTGCACACCTTCGGACATCCCAGGC  
 ACGAGGGTGTGCTGGATGTGGCCACACATAGGACCACACGTCCAGCTGGGAGGAGAGGCCT  
 GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT  
 TGGAAGATGCTGCTGAGTGTCTAAGCAGCACTGACAGCAGCTGGGCCGCCCCAGGGCAAC  
 GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTTGGAGCTGGGCTGCTGCTGC  
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
 GAGGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGAGGTCCGACAGCTGCGGGA  
 TGTGATTAAAGTCCCTGATGTTTCTC

**FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399  
><subunit 1 of 1, 157 aa, 1 stop  
><MW: 17681, pI: 7.65, NX(S/T): 1  
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDL P

**Signal peptide:**

amino acids 1-15

10017306.12101

**FIGURE 209**

AGCAGGAGCAGGAGAGGGACAAATGGAAAGCTGCCCCGTCCAGGTTTCATGTTCTTCTTTATTTCT  
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTCG  
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC  
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
 TAGCATGGTGCAAAATTTCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACATG  
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTTAGCCGTTTCATTGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGTGACTGTGATTGGGTTATTCAACAGCG  
 TAATTCAGATTTCATCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCGACCAAGCTCTTCCAGGGGAAGATTCTCTTTATCTGGTGGACAG  
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACATAAAGGAGTCTCAACTGCCAG  
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC  
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCCTAAGTGGAATAATGTTGAAGAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTTGACTTCTCCTTGGAACACATATGGCC  
 AAGTATCTACTTTATGCAAAAGTAAAAAGGCACAACTCAAATCTCAGAGACATAAACAACAG  
 GATCACTAGGCCTGCCAACCACACACACACGACGTGCACACACGACGACGCGTGCACAC  
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC  
 TTCTTCTCTTTTTAAATTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
 CCTCTATGAAGAGAGGCATTCCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGTCTCTTTAAGGTTACCTAAGGGT  
 TGAAACTCTACCTTCTTTTCATAAGCACATGTCGCTCTGACTCAGGATCAAAAACCAAGG  
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAATAGACCATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCC  
 TATGTAAATCAACAACCTGCATAATAAATAAAGGCAATCATGTTATA

**FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401  
><subunit 1 of 1, 273 aa, 1 stop  
><MW: 30480, pI: 4.60, NX(S/T): 1  
MEAPSRFMFLFLLTCELAEEVAAEEVKSSDGPAAQEPTWLTDPAAEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVVEHVQNF  
CDGFLSGKLLKENRESEKTPKVLE

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG  
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATG**CGACGCTCCGCCGGAGCCGGG  
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTGG  
 GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACC  
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTTCCACTACTC  
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG  
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
 TGTGCTAGAAAAAGAGAATTTCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
 CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACACAGTTAAGCAGGC  
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
 AGGGCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAAC  
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC  
 CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAAATGTAGCCCATTAACCATGT  
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
 ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA  
 TGAAGATGGTATGATTCTACATATGTACCATTTGTCTGTGTTTTGTACTTTCTTTTC  
 AGGTCATTTACAATTGGGAGATTTCAGAAACATTCTTTCCACCATCATTTAGAAATGGTTTG  
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG  
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA  
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
 AAATGTGTCATATCAATTTCTGGATTCTAATAGCAAGATTAGCAAAGGATAAATGCCGAAG  
 GTCACCTTCATTTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT  
 GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTA

**FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510  
><subunit 1 of 1, 269 aa, 1 stop  
><MW: 29082, pI: 9.02, NX(S/T): 3  
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNSKRDTGCTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSKINKSESVVYADIRKN

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

**FIGURE 213**

SCCGGCTGTGCAGAGACGCC**CATG**TACCGGCTCTGTGCAGCAGTGACTGCCCGGGGTGC CGCC  
CCCGGGGGCTTGCCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGTGCCGCC  
TCTCGGCCACGGCTGGGTGCGGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
TGGCAGGTGGGCTGAGGGGCGCGGCCCGGGCGCAGTCCCCGCGGCCCCGACCCGTGAGGCG  
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGAGACCCCGGC  
GCCGCCCTGTCTCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
TCAAGGATGAGGTGGGCGCACCGGCATAGTGGTGGAGTTTCTGTAGATGGAAGAAGACT  
TGGTCAGAAGTTTtagTTATGCTGATGTTGAGAACCCTGTACCATGTAACACAGAGACAGT  
TAGGCGAATTGCTAGCATCAGCAAAAGTCTACCATGGTGTGCTCTTGCCAAATTGTGGGAAG  
CAGGGAACCTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAA  
TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGAATTCTG  
TCATTATGAAAAGGACATAAAAAAGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAGGCAAAAGTAATGAAAAGAAATGATTTT  
ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAACCTGGCAAGAA  
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTAAAAATTCATTTGAAT  
CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGATTCA  
ACTTTTGGCTATACCCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAATATTTGGA  
CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
CAGTGATTTACAATAGAGCAAGGT**TAA**ATGAATACCTTCTGCTGTGCTAGCTATATCGCATC  
TTAAACATTTATTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAATCAACCTGC  
CAACTTTGGGAGCTTTTTCATAGTGTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACAA  
TGTTTATAAAGTAAAAAA



**FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522  
><subunit 1 of 1, 373 aa, 1 stop  
><MW: 41221, pI: 8.54, NX(S/T): 0  
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPSCSRCFARAIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

GTGACACTATAGAAGAGCTATGACGTGCGCATGCACGCGTACGTAAGCTCGGAATTCCGGTCC  
AGGCTGGTGGGAAGAAGCCGAGATGCGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGCAGCGGTGCCGGGCCGGGACT  
GGTGCGCAGGGGCTGGGCGGAAGGTCGAGAGGGCAGGCCGTGTGGCACGGTGGGGCTGCT  
GCTGGAGCACTCATTGTAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGCAGCTCAGCGAGGAGGAGCGGGGC  
CGACTCCGGGATGTGGCAGCCCTGAATGGCTGTACC GGCTCCGGATCCCAGGCGACCCGG  
GGCCCTGGATGGCTGGAAGCTGGTGGCTATGTCTCTCTTGTGCTCCTGCTGCTCCTTGG  
TGGAGTCGCACCTGTGCGACAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
GTGTCCGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACACAGCCCAGGCCCTGAGACGGCGG  
CCTTCATTGAGCGCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCGAGGAGCAGAAG  
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCTCTCATGATGTCAGG  
AGCGCCAGACACCCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
TTTGCTGTGTGCCACCCCTCCCTGTAAAGTCTATTAAAAACATCGACGATACATTGAAATGTC  
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCACTGTGTTTTGGCAAGACGG  
TCCTGATGTACAAGCTTGATTGAAATCTACTGCTCACTTGATACGTTATTTCAGAAACCCAG  
GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
TAAAGTGTCCCCAGATCGACACGCAAAAAA

**FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529  
><subunit 1 of 1, 269 aa, 1 stop  
><MW: 28004, pI: 5.80, NX(S/T): 1  
MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRPALDGLEA  
GGYVSSFVPACSLVESHLSQDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELNTSVQ  
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSF FAKYWYIIIPVVLFLMMSGAPDTGGQ  
GGGGGGGGGGGSGLCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGCAGCAGGTGCTCCGGGGGCCACC  
**ATG**TGTGGTGACTGCCTACCTTGCTTTTGTAGGCTCCTGGCCTCCTGCCTGGGGCTGGAAT  
GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCTGCAGCAATCCCTCCTTCCTTCGGTTT  
AATCGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
CTCTATAAACTCTACCAAGCATTACTACTTCTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
TGGCCTTGCCCTCTACAGTCCCTTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGT  
GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT  
CAAGACTACTTTGTGCTGTAGTGGGGCAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
CTCAGCCTTCGAGGCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCGCTGTAGTGGCAGGT  
GTGGCAGCTGAGGCTGTAGCCAGCTGGAATAGGGCTTGGGCTGTAGGCCCCCTTTGTGGCTGC  
CATGCCCTTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAATATGACC  
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCGCTGCCTCCTGTCTGGACCGCCG  
GTGCTGCTGCTGGGACCATACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCTCT  
CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCTTCTCTCTCTTCATGTTGACTTT  
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCTTCATAGCCTTTCTACTTATTGAGT  
TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA  
GAGCAGGCTGGTGACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTCAGCATTGTGCTCTG  
CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGGTAAGGCATGATGCT  
GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG  
GACAAGATAGCTGGGACAGACTCTTGAAATCCAGCTATCCGGGATTGACGAGCTCTCTGT  
GACTGACTTTTGACTGTCTGTGGTTTCTCCTGCCATTCCTTGTGTTTGGAGGACATGA  
TGGGGGTGATGGACTGGAAGAAGGTTGCCAAAAGTTCCTCTGTGTTACTCCATTAGAAA  
ATAAACACTTTTAAATGATCAAAAAAAAAAAAA

**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAIPLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFSPMSFLRRKVIPET  
EQAGVLNWFVRVPLHSLACLGLLVLHSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA  
ELRVPSPTTEFPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430



**FIGURE 220**

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHIDYLFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPEAPEACGELSGNFFIQDQIALVERGCGSFLSKTRVVQEHGGRAVVISDNAVNDNSF
VEMIQDSTORTADIPALFLLGRDGYMIRSLLEOHGLPWAIISIPNVNVTISIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCAC TGCTGTGTGGGCTGGTGGTGA  
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
ACTGGGAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG  
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC  
TGAAGACCCAGGGGTGCGGCATCTACAAGACAACAACAAAGCAGCATACATTGTATGGAT  
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAATGAGGACTC  
CGAA**TAA**AAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA



**FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGIILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFENVYILENEDSE
```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCCCAGGGGGCCCCAGGAGAGTATAAAGGCGATGTGGAG  
 GGTGCCCCGGCACAAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG  
 CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
 GGCCCTGGAGGAGGCAAGTATTTAGCACCACCTGAAGACTACGACCATGAAATCACAGGGCT  
 GCGGGTGTCTGTAGGTCTTCTCCTGGTAAAAAGTGTCAGGTGAAACTTGAGAGACTCCTGGG  
 ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC  
 ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
 GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
 AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
 TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
 AGCAAACCTACCCGTGGGTGCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
 GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
 AATAAAGCTTCTGCAGAAAA

**FIGURE 224**

Signal peptide:  
amino acids 1-22

Signal peptide:  
amino acids 1-22

**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAACTGGGTGCTCATCACGGGAAGCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGGCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGAGGATCCAGTT  
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
 TATTGTGTTCTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAAATCGGTCCATCT  
 CCCAAGGGGTCCAATTTTTCTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGGCTGTGATGCACTGGCCCCTAAGCCAAGCAAAAGACCTAAGGACGACCTTTGAA  
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTGCCTATAACAGCCTTCAAAAACCTAAGTATAAT  
 CAATTTAAAGGGCTCAACGAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAAATGGAATACGAGACTCAAAGAGCTGATTCCTTAGTTCCAATAGAA  
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCAGGAGCTGCTGAGTTT  
 ACATTTACGGTCTAATCCTCTGAGAACCATCCTCTGTGCGAATATTTCAAAGACTGCCGCAAC  
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGCTTTGCTGGC  
 ATGATCAGACTCAAAGAACCTTCACCTGGAGCACAATCAATTTTTCAAAGCTCAACCTGGCCCT  
 TTTTCAAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCACTGGAATAAAATCAGTGTATAG  
 GACAGACCATGCTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC  
 GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGGCTCAACCTGGA  
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA  
 TCAGTCTTGCTGGGAATATATGGAATGCAGCAGAAATATTGCTCCCTTGTAACCTGGCTG  
 AAAAGTTTTAAAGGCTAAGGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
 AGTAAATGTATCGATGCACTGAAGAAGTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT  
 GAGAGCAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG  
 TGCTCGTCATCCTGCTGGTTATCTACGTGTGATGGAAGCGGTACCTGCGAGCATGAAGCAG  
 CTGCAAGCAGCGCTCCTCATGCGAAGGCACAGGAAAAAGAAAGACAGTCCCTTAAGCAAAAT  
 GACTCCCAGCACCCAGGAATTTTATGTAAGTTATAAACCCCAACACAGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
**TGA**ACCATTTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAACCTC  
 TGGTGACTATCAAGGGAACGCGATGCCCCCTCCCTTCCCTCTCCCTCTCATTGTTGGTGG  
 CAAGATCCTTCTCTGTCCGTTTTAGTGCATTATAATACTGGTCATTTTCTCTCATACATA  
 ATCAACCCATTGAAATTTAAATACCACCAATCAATGTGAAGCTTGAACCTCCGGTTTAATATAA  
 TACCTATTGTATAAGACCTTTTACTGATTCATTAATGTGCAATTTGTTTTAAGATAAAACT  
 TCTTTCATAGGTAAAAAATAA

10017305.22101

**FIGURE 226**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTIVLLTMLSSAERGCPKGCRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNFTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQNLYLQWNKISVIGQTM
SWTWSSSLQRLDLSGNEIEAFSGPSVVFQCVPNLQRLNLDNKLTFFIGQEILDLSWISLNDISLA
GNIWEC SRNICSLVNWLKSFKGLRENTIICASPKEIQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTC TGAGAAAGAAGGAAATAAACACAGGCACCAAACCCTATCCTAAGTTGACTGTCCTT  
 TAAAT **ATG**TCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG  
 TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
 AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCCTGCTCCAGTGTGGCTGAGGAGACCCCGA  
 ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTCTGTGGAGACTTGGACTCTATTTATGG  
 GACAGAAGCAGCTGTGAGTCCAACCTGTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
 ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
 AAAACAACCT**TGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
 AACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAATGTCCAGAGATCTATTTCATATA  
 GTCTGAGGAAGGACAAATTCGACAAAAGAATGGATGTTGGAATAATTTTGGTCATGGAGATG  
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
 TCCATCAGATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
 CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
 GTCCAGAACCAGAACCAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
 CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATGTAGATAGAAGGTGA  
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAAGAAATTTCCC  
 CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTCCTCTGGAGCCTCAGGGCTTG  
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
 CAAAAACATCCATCAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAT  
 AACATCAATAGATATCTAAAAA

**FIGURE 228**

```
>>/usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA77303
>>subunit 1 of 1, 146 aa, 1 stop
>>MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSIAISTIGILCLPLFLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGLGLSPPPYIEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

**FIGURE 229**

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCACTCCCACCCACCGGCGT  
 TTCCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCGAGCTGACGCCCCGCTTATTA  
 GCTCTCGCTCGCTCGCCCCGGCTCAGAAGCTCCGTGGCGCGCGCGACCGTGACGAGAAGCCCC  
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT  
 CCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACTTGTCTGAAG  
 ATGAAGAATAACAAATATTGAGGATATTTTTTCTTTTTTTTCAAGTCTTGATTGTGGC  
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTGCTTCTTCAGAAATGTTTTTTA  
 CAATCTCAAGAAAAATATGTCCAGAAATGAGTTTACTGTTGCTTGTATTGGGACTCATT  
 TGGGATTTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAAATACAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT  
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
 TGTGTGAATGGCTCAGCAGCCAAACCCCAATGGTATGTGGGAAATTTGGTGCCAGTAA  
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTATGGAAC  
 TCTAATTCGTACATAAAAATTTTAAAGTTATTTGTTTTCAGGCAAGTCTGTCTCAATG  
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACATGAAAACATGGATT  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA  
 TCATTCGTCTATTTGTTCTCAATAGATGTAACCTGTAGACTACGGCTATTTGAAAAAATGTG  
 CTTATTGTACTATATTTTGTATTCCAAATTTAGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTGCACTATCCTTCAGAATAACTGA  
 AGGTTAATTATGTATATTTTAAAAAATACACTTATAAGAGTATAATCTTGAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAATAGTT  
 GTAACCTCTAATCTTATACTTATGGAAGAATAAAGATATTTTTATGATGAGAGTAACAATA  
 AAGTATTTCATGATTTTTTACATACATGAATGTTTCAATTTAAAAGTTTAAATCCTTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGACCTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA  
 GGTACTTTTGTGCTGCATTAAATGCTTGGAAAGTGTAAACATTATATTATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAGTGGCAC  
 TTTAAATAAGAACATTTAAATATAAATATGAAGATTGACTATCTTTTCAGGAAAAAAGCT  
 GTATATAGCACAGGGAACCCATAATCTTGGGTAATTTCTAGTATAAAACAAATTTACTTTTAT  
 TTAATTTCCCTGTAGCAAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTTAT  
 CTCATATAGTAGCTCTTAAGTGCAGCTAGCTTCTAGATTAGACTATAGCAATTTAGATAT  
 TGTATTGTTCTGTCATTATATATGCTACCACATGTAGCAATAATCAATATTTTATTAAAA  
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTTCTCTCTCTGTA  
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGGCAGGT



**FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTNGTSGNL
VPVTTNKRTNVSGSIR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**FIGURE 231**

CGCGGCCGGGGCCGCCGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCCATGCT  
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCCTTTTCGACAGCTTCAGCCTGACTCGG  
 GTGGATTGTAGCGGCTGGGCCCCACATCATGCCGGTGGCCATCCCTCTGGACACAGCCCA  
 CTGAGACCTGTCTCCAAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCGGGGCT  
 ACACGACGTTGGCTGGCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCATGCCC  
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
 AGCCGAGAGCTTACCAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG  
 AGGTCTCAGTGTCTGCCCTTACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC  
 CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCACCAT  
 TCAGAGCCTGAACCTGGCCTGGAAACCGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
 TGCGCTACCTGAGCCTGGATGGAAACCTCTAGCTGTCAATGGTCCGGGTCCCTTCGCGGGG  
 CTGGGAGGCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTTGACCTTGCGGCAACCCCAAGCTTAACT  
 GGGCAGGAGCTGAGGTGTTTTCAGGCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
 AACCTGGTGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
 GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGGGGAGGGGCACTACCCCGGAGGCGTGGCT  
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC  
 ATCTT**TGTA**CAAAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTTGGGCTGCCTCAG  
 GTCCCCAGTAACTTATGTTCAATGTGCCAACACCAAGTGGGGAGCCCGCAGGCCATATGGGCA  
 CGCTCACCACAGGAGTTGTGGGCTAGGAGAGGCTTTGGACCTGGGAGGCCACACCTAGGAGC  
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGATTCGATGCCA  
 AACACAGACTCGGGTCCCTCCTGCTTCCCTTCCCCACCTTATCCCCAAGTGCTTCCCTCAT  
 GCCTGGGCGGGCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
 GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT  
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCTTTTCTAT  
 TTCCCTAGAACCTTAAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCTTCTCATGTGAC  
 AGATGGGGAACACTGAGGCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
 ATGACTGGAGCACAGCTTCCTGCCTCCCAGCCCGGACCCAATGCATCTTCTTGTCTCTCTA  
 ATAAGCCCCACCTCCCGCCTGGGCTCCCTTGTGCCCTTGCTGTTCCCATTAGCACACA  
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAAGTGGGACTCTGGGCTCTGCACAGCT  
 GTGCGCATGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGACATATGGTT  
 CCAGCCTAGCCAGTTTCTCACCTGGGTTGGGGTCCCCAGCATCCAGACTGGAAACCTACC  
 CATTTTCCCTGAGCATCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
 TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTCACTCCCACTGGCCCTGAGCAGCAGCAGC  
 CCTTCTTACCTCCAGGAATGCCGTAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC  
 TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCCCTTAGTCTTCATTTTA  
 TAAAGTTGTGCTTTTCTAACGGAGTGTCACTTCAACCGGCTCCCTGCTACCTGCTGGC  
 CGGGGATGGAGACATGTCAATTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACCTTTTGAAT  
 ATTGTCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGCTCTTCCCCACCTGCCATGC  
 CCATCATCTATCTAACCGGTCTTGATTAAATAAACACTATAAAAGGTTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

10017306.123101

**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652  
><subunit 1 of 1, 353 aa, 1 stop  
><MW: 37847, pI: 6.80, NX(S/T): 2  
MPWPLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH  
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP  
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPT I  
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGTLHLSLASLQRLPELAPS  
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPPLPEALLHLPALQSVSV  
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCTCCCCAGTTCCTGTGGGTCTGAGG  
 GGACCAGAAGGGTGAGCTACGTGGCTTTCTGGAAGGGGAGGCTAT**TATG**CGTCAATCCCCA  
 AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
 GTTCCAGGCCCTTACCTGCTGGGCACCTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCAC  
 GGGAGGCTTGGCAGTTTTTCTTACTCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC  
 TCTAGTCTTGCCTTCAGCCTTCTCTGTCTGCGTTTTATCTCTATGGACTCCTTCCACTGG  
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATGCCACAAACCTTCAGGAAATACGAAATG  
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA  
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACCTCTCC  
 GGAAGATCAGCAGCCTCGCCAATTCCTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTTGAAAAGCTGGAAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC  
 TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT  
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTACT  
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGAT  
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTGTGATAAGATTTTGTAAATATCTT  
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGGCTATTTAATGTATTT  
 ATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTTATACAGTAAAAAAAAAAACCTTGTAAATCTAGAAGAGTGGCT  
 AGGGGGTTATTCACTTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
 TATTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT  
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
 CTTCCAGCCAGGAATCCTACAGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATA  
 CCAAAAAAAAAAAAAAAAAA

**FIGURE 234**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261.aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSLFTIKKDLRLSHAMTCHCGEEAMKKYSQILSHFEKLEPQAQAVVKALG
ELDILLQWMEETE
```

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGAGAGGCTTTTGCCG  
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC  
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
 CTCTTGCTCGGTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA  
 GCCCTAGGGATCATTTGAAGAGGAAGGCTTTCTAAGCTTTGGCAAGGAGTGACACCCGCCAT  
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG  
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTCAGATGCAAAT  
 GGAAGGAAAAGGAACTGGAAGGAAAACCATTGCGATTTCTGGTGTACATCATGCATTTG  
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAACACTACTTGGT  
 ATTGAATACACCCTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA  
 CGAGATAAACAAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT  
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTGGCTGAGAATGACCC  
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
 TTTTAA

**FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568  
><subunit 1 of 1, 323 aa, 1 stop  
><MW: 36064, pI: 9.33, NX(S/T): 1  
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDA  
RESAPYRGMVRTALGIEEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEH  
YPLWKSIVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEKPLRFRGVHHAFKILAEGGI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT  
YEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

1001-2001-3001-4001-5001-6001-7001-8001-9001-10000

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCTGCGCGCGC  
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
 TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGCAGGTATATTGTTTTTACAGGC  
 TGGTGGATAATGATTGATGCGAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
 TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC  
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
 TTCATTGGTTTCATGTTGATGTTTGGGTCACCTTATTGCTTCCATGTGGATTCTTTTTTGGTGC  
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA  
 TATTTTTTAGCACTCTGATCTACAAAATTTGGAAGAACCAGAGAGCTATGGACCTGAGATCAC  
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTATCTCTCAGT  
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTATGTTC  
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTA  
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA  
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTGTAGAAGTAACCACTCTTGT  
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGCGGG  
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT  
 AAAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
 TGAGGCAGGAGAATCGCTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
 TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
 TAAAAGGTTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA  
 AAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC  
 AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA



**FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

**Important features:****Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

**FIGURE 239**

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAAGCTGGCCAGGGTGGT  
 GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAAGCTGACCCCAAGCCACCCTTACCTGGACAG  
GATGAGAGTGTCAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
 TGTTTATTGGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
 AGCCAACTACTTTGCGTTTAAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCATAACATC  
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATCCGGGGGGTGCACCTGGTGTGGTGG  
 CCTCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTGACTTG  
 GGGAGTTCTACGCAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTTTAGGGTGGC  
 TGTGGCTCTTCTCAGCCAGGGGCCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG  
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCTGGAAGGTGCTGCAGGTCTTGACGCG  
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCCTCCACAGCACATCCTACCCGGAAGACC  
 AGCCTCAGAGGGTCTTCTGGAACAGCTGTCTGTGGAGAGAATGGGTGCTTTCTGTCAGGG  
 ACTGCTGACGGCTGGTCTGAGGAAGGACAAACTGCCCAGACTTGAGCCCAATTAATTTTA  
 TTTTGTCTGGTTTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKEYEGWPELLEMEGCMPPKPF
```

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

7663 7664 7665 7666 7667 7668 7669 7670 7671 7672 7673 7674 7675 7676 7677 7678 7679 7680 7681 7682 7683 7684 7685 7686 7687 7688 7689 7690 7691 7692 7693 7694 7695 7696 7697 7698 7699 7700 7701 7702 7703 7704 7705 7706 7707 7708 7709 7710 7711 7712 7713 7714 7715 7716 7717 7718 7719 7720 7721 7722 7723 7724 7725 7726 7727 7728 7729 7730 7731 7732 7733 7734 7735 7736 7737 7738 7739 7740 7741 7742 7743 7744 7745 7746 7747 7748 7749 7750 7751 7752 7753 7754 7755 7756 7757 7758 7759 7760 7761 7762 7763 7764 7765 7766 7767 7768 7769 7770 7771 7772 7773 7774 7775 7776 7777 7778 7779 7780 7781 7782 7783 7784 7785 7786 7787 7788 7789 7790 7791 7792 7793 7794 7795 7796 7797 7798 7799 7800 7801 7802 7803 7804 7805 7806 7807 7808 7809 7810 7811 7812 7813 7814 7815 7816 7817 7818 7819 7820 7821 7822 7823 7824 7825 7826 7827 7828 7829 7830 7831 7832 7833 7834 7835 7836 7837 7838 7839 7840 7841 7842 7843 7844 7845 7846 7847 7848 7849 7850 7851 7852 7853 7854 7855 7856 7857 7858 7859 7860 7861 7862 7863 7864 7865 7866 7867 7868 7869 7870 7871 7872 7873 7874 7875 7876 7877 7878 7879 7880 7881 7882 7883 7884 7885 7886 7887 7888 7889 7890 7891 7892 7893 7894 7895 7896 7897 7898 7899 7900 7901 7902 7903 7904 7905 7906 7907 7908 7909 7910 7911 7912 7913 7914 7915 7916 7917 7918 7919 7920 7921 7922 7923 7924 7925 7926 7927 7928 7929 7930 7931 7932 7933 7934 7935 7936 7937 7938 7939 7940 7941 7942 7943 7944 7945 7946 7947 7948 7949 7950 7951 7952 7953 7954 7955 7956 7957 7958 7959 7960 7961 7962 7963 7964 7965 7966 7967 7968 7969 7970 7971 7972 7973 7974 7975 7976 7977 7978 7979 7980 7981 7982 7983 7984 7985 7986 7987 7988 7989 7990 7991 7992 7993 7994 7995 7996 7997 7998 7999 8000 8001 8002 8003 8004 8005 8006 8007 8008 8009 8010 8011 8012 8013 8014 8015 8016 8017 8018 8019 8020 8021 8022 8023 8024 8025 8026 8027 8028 8029 8030 8031 8032 8033 8034 8035 8036 8037 8038 8039 8040 8041 8042 8043 8044 8045 8046 8047 8048 8049 8050 8051 8052 8053 8054 8055 8056 8057 8058 8059 8060 8061 8062 8063 8064 8065 8066 8067 8068 8069 8070 8071 8072 8073 8074 8075 8076 8077 8078 8079 8080 8081 8082 8083 8084 8085 8086 8087 8088 8089 8090 8091 8092 8093 8094 8095 8096 8097 8098 8099 8100 8101 8102 8103 8104 8105 8106 8107 8108 8109 8110 8111 8112 8113 8114 8115 8116 8117 8118 8119 8120 8121 8122 8123 8124 8125 8126 8127 8128 8129 8130 8131 8132 8133 8134 8135 8136 8137 8138 8139 8140 8141 8142 8143 8144 8145 8146 8147 8148 8149 8150 8151 8152 8153 8154 8155 8156 8157 8158 8159 8160 8161 8162 8163 8164 8165 8166 8167 8168 8169 8170 8171 8172 8173 8174 8175 8176 8177 8178 8179 8180 8181 8182 8183 8184 8185 8186 8187 8188 8189 8190 8191 8192 8193 8194 8195 8196 8197 8198 8199 8200 8201 8202 8203 8204 8205 8206 8207 8208 8209 8210 8211 8212 8213 8214 8215 8216 8217 8218 8219 8220 8221 8222 8223 8224 8225 8226 8227 8228 8229 8230 8231 8232 8233 8234 8235 8236 8237 8238 8239 8240 8241 8242 8243 8244 8245 8246 8247 8248 8249 8250 8251 8252 8253 8254 8255 8256 8257 8258 8259 8260 8261 8262 8263 8264 8265 8266 8267 8268 8269 8270 8271 8272 8273 8274 8275 8276 8277 8278 8279 8280 8281 8282 8283 8284 8285 8286 8287 8288 8289 8290 8291 8292 8293 8294 8295 8296 8297 8298 8299 8300 8301 8302 8303 8304 8305 8306 8307 8308 8309 8310 8311 8312 8313 8314 8315 8316 8317 8318 8319 8320 8321 8322 8323 8324 8325 8326 8327 8328 8329 8330 8331 8332 8333 8334 8335 8336 8337 8338 8339 8340 8341 8342 8343 8344 8345 8346 8347 8348 8349 8350 8351 8352 8353 8354 8355 8356 8357 8358 8359 8360 8361 8362 8363 8364 8365 8366 8367 8368 8369 8370 8371 8372 8373 8374 8375 8376 8377 8378 8379 8380 8381 8382 8383 8384 8385 8386 8387 8388 8389 8390 8391 8392 8393 8394 8395 8396 8397 8398 8399 8400 8401 8402 8403 8404 8405 8406 8407 8408 8409 8410 8411 8412 8413 8414 8415 8416 8417 8418 8419 8420 8421 8422 8423 8424 8425 8426 8427 8428 8429 8430 8431 8432 8433 8434 8435 8436 8437 8438 8439 8440 8441 8442 8443 8444 8445 8446 8447 8448 8449 8450 8451 8452 8453 8454 8455 8456 8457 8458 8459 8460 8461 8462 8463 8464 8465 8466 8467 8468 8469 8470 8471 8472 8473 8474 8475 8476 8477 8478 8479 8480 8481

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCCAAAGAGGCAGCAAGAGATTTGTCTCTGGGGATCCAGAAACCCCATGATACCCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAAATACACTACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCTACTCTCCCTCCCTCTCTCTCTGCTGTCTTAGTCTCTAGTCTCTCAAATCCCAGTCCCCTGCACCCCTTCTCTGGGACACTATGTGTGTCTCCGCCCTCTCTGCTGGAGGTGATTGGATCCGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCAACCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTACAGACAGACAGTGTGACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCCGAGCCTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCATGGGGTCAGAAAGGATCCCCAGGGGGTGCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTTGATATTATGACTCTGATTTCTTATGACAGCTTGAGTGAGGCTGCTGAGAGGCTCAGGCGCTGGCTGTCTCTGGGCATCCTAATTGAGTGGGTGAGACTAAGAATATAGCTTATGAACACATTTCTGAGTCCCTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCCTTCAACCTAAGAGAGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCAGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCTGGCTGTTTATTTCATTGCTAGAAAGATTCCGAAGAAGAGGCTGGAAAACCGAAGAGTGTGGTCTTCACTCAGCACAAGCCACGACTGAGGCATTAATTCTCTCGATACCATGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTATAGAGGAATGGACCCAGGCTGTCATTCCAGGAAGAAGTCGACAGCCTTCAGCCTCCCAACAGTGGAGGAAATGAGGAAATCGCTGTCTTGTTTAATCGCAGACCAACTCTGTTTAGTTGAGGGGGAAGTTTGGGATATACCCCAAGTCTCTTACCCCTCAGTNTTATGGCCCTTCCCCTAGATATACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTGGAAATTAAAGTTTCTGACTTT

**FIGURE 242**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

**FIGURE 243**

AATTTTTTACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC  
 GTGGACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGTCTTCTAGG  
 ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCACAAAACCTGGCTC  
 CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG  
 ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG  
 AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC  
 TGCACCCACATGTGTTACCAATTTTTGTACACAACTTGAGCCCAGGGCACTATCCTAAGC  
 TCAGAGGAATTGCCCAAATCTTCACGAGCCTCATCATCCATTCTCTGTTCCCGGGAGGCAT  
 CCTGCCACCAGTCAGGCGAGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG  
 GAGCAGGTGTAATCCTGCCACCCAGGGAACCCAGCAGGCCGCTCCCACTCCCAGTGGC  
 ACAGATGACGACTTTGCACTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA  
 GGAAGCCACCACAGAATCAGCAAATGGAATTCAGTAAGCTGTTTCAAATTTTTCAACTAAG  
 CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATATGGAATAGATTGA  
 GACACATTGGATAGTCTTAGAAGAAATTAATCTTAATTTACCTGAAAATATTTCTTGAATTT  
 TCAGAAAATATGTTCTATGTAGAGAATCCCACTTTTAAAAACAATAATTCAATGGATAAAT  
 CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTTAAACATATTTGAAA  
 ACTGGAA  
 AAAAAAAAAAAAAAAAAAAAA

**FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGGLNVQQQLHHPVLPFI FVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

1001-200-222111

**FIGURE 245**

GGAGAGAGAGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGAGCGCGCGG  
GAGCCAGACGCTGACCACGTTCTCTCTCTGGTCTCTCTCGCCTCCAGCTCCGCGCTGCCCG  
GCAGCGGGGAGCCATGCGACCCAGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCC  
TGCTGCTCTGCTGCTGCAGCTGCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAG  
GCCAGCAGGAGTGCTGGTCGAGACGGGAGCCCTGGGGCCAAATGTTATCCGGGTACACCTG  
GGATCCCAGGTGCGGATGGATTCAAAGGAGAAAGGGGAATGTCTGAGGGAAGGCTTTGAG  
GAGTCTGGACACCAACTACAACAGCATGTTCTGAGGTTCATTGAATTAATGGCATAAGTCT  
TGGGAAAAATTCGGGATGTACATTTACAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
TCAGTGGCTCACTTCGGCTAAAAATGCAGAAATGCATGCTGTGACGTTGGTATTTACATTTC  
AATGGAGCTGAATGTTCAGGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
CCCTGAAATGAATTACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
GAATTGGTGTGATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTGAGATTACCCAAA  
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTGCGCATATTATTGAAGAACTACCAAAATA  
AATGCTTTAATTTTCATTGTCTACCTCTTTTTTTTATTATGCCCTTGAATGGTTCACTTAAAT  
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCAATTTGCTTCAATCAAAAGT  
GGTTTCAATATTTTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCTCAACCTA  
TAATTTGGAATATTGTTGTGGTCTTTGTTTTTCTCTTAGTATAGCATTTTAAAAAATA  
TAAAGACTACCAATCTTTGTACAATTTGTAAGTGTAAAGATTTTTTATATCTGTTAAAT  
AAAAATTATTTCCAACA



**FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393  
><subunit 1 of 1, 243 aa, 1 stop  
><MW: 26266, pI: 8.43, NX(S/T): 1  
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV  
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

2001-06-22 10:10:10